

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*  
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched.  
Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or  
utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if  
known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
jan.delaval@uspto.gov

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) <u>✓</u>	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) <u>✓</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>8/26/02</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>8/26/02</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>✓</u>
Clerical Prep Time: <u>15</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>15</u>	Other _____	Other (specify) _____



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 15:00:21 ; Search time 1863.47 Seconds  
(without alignments)  
4548.100 Million cell updates/sec

Title: US-09-249-011-5  
Perfect score: 405  
Sequence: 1 atgggttggaactgatac.....cccttgacccgctcctca 405

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
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17: em\_hum:\*  
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19: em\_mu:\*  
20: em\_om:\*  
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22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
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27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
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1	289.6	71.5	805	12	AF239196	AF239196 Synthetic
2	272.2	67.2	446	6	I08288	I08288 Sequence 4
3	272.2	67.2	462	10	S78361	S78361 AH1107 VH r
4	265.8	65.6	1767	6	E40699	E40699 Antihuman F
5	265.8	65.6	1768	6	E40700	E40700 Antihuman F
6	254.4	62.8	424	6	AR174947	AR174947 Sequence
7	253.6	62.6	451	6	AR144016	AR144016 Sequence
8	253.6	62.6	2071	6	E40080	E40080 Drug contai
9	253.6	62.6	2071	6	E40888	E40888 Humanized a
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12	252	62.2	2073	6	E40911	E40911 Humanized a
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15	248.8	61.4	457	6	E40042	E40042 Drug contai
16	248.8	61.4	457	6	E40850	E40850 Humanized a
17	248.8	61.4	457	6	E43396	E43396 Humanized a
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20	248.8	61.4	2077	6	E43409	E43409 Humanized a
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22	248.2	61.3	433	6	AR045196	AR045196 Sequence
23	248.2	61.3	433	6	BD011420	BD011420 Chimeric
24	248.2	61.3	433	6	E43890	E43890 Chimeric
25	245.6	60.6	2077	6	E43441	E43441 Humanized a
26	245	60.5	405	6	AR126855	AR126855 Sequence
27	245	60.5	405	6	I31950	I31950 Sequence 68
28	245	60.5	405	6	I78562	I78562 Sequence 68
29	245	60.5	405	6	I78617	I78617 Sequence 68
30	245	60.5	405	9	HSBUD114H	Z46348 Homo sapien
31	245	60.5	405	10	MUSIGHM195	M83098 Mus muscullu
32	243.4	60.1	405	6	E16346	E16346 DNA encodin
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35	241.8	59.7	451	9	AF062257	AF062257 Homo sapi
36	241.8	59.7	451	10	MUSANTYDJ	M37621 Mouse anti-
37	241.8	59.7	471	10	MUSIGHPG	M27788 Mouse Ig ac
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39	241.2	59.6	700	10	MUSIGHAM	M25465 Mouse Ig re
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41	240.2	59.3	406	10	MUSIGHMX	M28251 Mouse Ig re
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44	239	59.0	418	6	E16328	E16328 DNA coding
45	239	59.0	418	6	E16335	E16335 DNA coding

ALIGNMENTS

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AF239196 LOCUS 805 bp mRNA linear SYN 03-JUL-2000  
DEFINITION Synthetic construct BCL1 lymphoma-derived single chain idliotype  
ACCESSION AF239196  
VERSION AF239196.1 GI:8925314  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequence.  
REFERENCE 1 (bases 1 to 805)  
AUTHORS Schreurs,M.W.J., van den Berk,P.C.M., van Oers,M.H.J. and Kersten,M.J.  
TITLE Murine BCL1 lymphoma-derived single chain antibody (scFv) sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 805)  
AUTHORS Schreurs,M.W.J., van den Berk,P.C.M., van Oers,M.H.J. and Kersten,M.J.  
TITLE Direct Submission  
JOURNAL Submitted (24-FEB-2000) Immunology, The Netherlands Cancer Institute, Plemanlaan 121, Amsterdam 1066 CX, The Netherlands  
FEATURES Location/Qualifiers

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/tissue\_type="Bcl1 lymphoma"  
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ORIGIN

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Best Local Similarity 83.6%; Pred. No. 1.6e-81;  
Matches 341; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

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DB 70 GTCCAGCTGCAGCAGTGTGGGCTGAGAGTGTGAGGCTGGGGCTCAGTGAAGATTTC 129  
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QY 121 tgcgaagcttcgagctacacattcactgattatgctatacagtggtgagagagctcct 180  
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DB 130 TGCAGAGGTTCCGGCTACATTCATGATTATGCTATGCACTGGTGAAGCAGATCAT 189  
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QY 181 ggaacaggtcctgagtgatgagtgatgagtgatgagtgatgagtgatgagtgatgag 240  
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DB 190 GCAAGAGTGTAGAGTGTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATT 249  
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QY 241 cagaagcttaagggcagaagcacaatgactgtagaagaagcagaagcagaagcagctatg 300  
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DB 250 CAGAAGTTTAAGGCAAGGCCACATGCTGATGACAAATCTCTCACACAGCTTATATG 309  
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QY 301 gaacttagtctctgagatctgagagatagagagagagagagagagagagagagagag 357  
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DB 310 GAACCTGCCAGATTGACATCTGAGAGATTCTGCCATCTATTACTGCAAGTACTATTG 369  
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QY 358 tggatatagtactgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 405  
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DB 370 AACTACTTTGACTGCTGGGGCAAGGCCACCTCTACAGTCTCTCTCA 417  
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RESULT 2  
LOCUS 108288 446 bp linear PAT 02-DEC-1994  
DEFINITION Sequence 4 from Patent EP 0380068.  
ACCESSION 108288  
VERSION 108288.1 GI:589000  
KEYWORDS  
SOURCE unknown.

ORGANISM Unknown  
REFERENCE 1 (bases 1 to 446)  
AUTHORS Zerler,B.D.  
TITLE An expression system for production of chimeric monoclonal  
antibodies  
JOURNAL Patent: EP 0380068-A1 4 01-AUG-1990;  
FEATURES  
source location/Qualifiers  
1. .446  
/organism="unknown"  
BASE COUNT 117 a 110 c 113 g 106 t  
ORIGIN

Query Match 67.2%; Score 272.2; DB 6; Length 446;  
Best Local Similarity 81.2%; Pred. No. 5.3e-76;  
Matches 322; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

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DB 45 ATGGGTGAGCTGTATCATCTTCTTCTGTAGCAACAGCTACAGGTGTCACCTCCAG 104  
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QY 61 gtccagctgtgcaactgtgagctggaagctggaagctggaagctggaagctggaagctgctc 120  
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DB 105 GTCCAGCTGCAGCAGTGTGGGCTGAGAGTGTGAGGCTGGGGCTCAGTGAAGATTTC 164  
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QY 121 tgcgaagcttcgagctacacattcactgattatgctatacagtggtgagagagctcct 180  
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DB 165 TGCAGAGGTTCCGGCTACATTCATGATTATGCTCTGCACCTGGTGAAGCAGATCAT 224  
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QY 181 ggaacaggtcctgagtgatgagtgatgagtgatgagtgatgagtgatgagtgatgagtgatgag 240  
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DB 225 GCAAGAGTGTAGAGTGTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATT 284  
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QY 241 cagaagcttaagggcagaagcacaatgactgtagaagaagctggaagcagaagcagctatg 300  
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DB 285 CCGAGGTTTAAGGCCAAGGCCACATGACTGTACAAATCTCTCACACAGCTTATATG 344  
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QY 301 gaacttagtctctgagatctgagagatagagagagagagagagagagagagagagagagagag 360  
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DB 345 GAACCTGCCAGATTGACATCTGAGAGATTCTGCCATCTATTACTGTGCAAGA---GGAAGC 401  
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QY 361 tatatgactactgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 405  
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DB 402 AACCTTGACTAGCTGGGGCAAGGCCACCTCTACAGTCTCTCTCA 446  
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RESULT 3  
LOCUS 578361 462 bp mRNA linear ROD 07-MAY-1993  
DEFINITION AHT107 VH region-chimeric mouse/human MAb against the human p55  
IL-2R heavy chain variable region [mice, mRNA Recombinant Partial,  
462 nt].  
ACCESSION 578361  
VERSION 578361.1 GI:243052  
KEYWORDS  
SOURCE  
ORGANISM Mus sp.  
MUS SP.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 462)  
AUTHORS Rose,B., Gillespie,A., Wunderlich,D., Barbosa,J.A., Cahill,K.,  
Dzubia,V., Shedd,D. and Zerler,B.  
TITLE A chimeric mouse/human anti-IL-2 receptor antibody with enhanced  
biological activities  
JOURNAL Mol. Immunol. 29 (1), 131-144 (1992)  
MEDLINE 92114885  
REMARK Genbank staff at the National Library of Medicine created this  
entry [NCBI g1bseq 78361] from the original journal article.  
This sequence comes from Fig1B.  
location/Qualifiers  
1. .462  
/organism="Mus sp."



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BASE COUNT 122 a 112 c 118 g 110 t

ORIGIN

Query Match 67.2%; Score 272.2; DB 10; Length 462;  
Best Local Similarity 81.2%; Pred. No. 5.3e-76;  
Matches 329; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

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DB 61 ATGGGCTGGAGTGTATCTCTCTTCTGGCAGCAACAGCTCAAGTGTGCTCCAG 120  
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QY 181 gtacagagcctcgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240  
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DB 241 GCAGAAAGCTGAGAGTGTGAATATTAGTCTTACATGTGTATCAACCTACAC 300  
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DB 361 GAACCTGCGCAGATTGACATCTGAAGATCTGCCATCTATTACTGTGCAAGA---GGAAGC 417  
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QY 361 tatatgactactgtgggtcaaggtacccctgtcacgcgtctctca 405  
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DB 418 AACCTTGACTACTGGGGCCAGGACCACTCTCACAGTCTCCCA 462

RESULT 4  
E40699 1767 bp DNA linear PAT 31-JAN-2002  
LOCUS  
DEFINITION Anthuman Fas humanized antibody-containing antirheumatic.  
ACCESSION E40699  
VERSION E40699.1 GI:18627288  
KEYWORDS JP 2000154149-A/70.  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequence.  
1 (bases 1 to 1767)  
AUTHORS Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.  
TITLE Anthuman Fas humanized antibody-containing antirheumatic  
JOURNAL Patent: JP 2000154149-A 70 06-JUN-2000;  
SANKYO CO LTD  
OS Artificial Sequence  
PN JP 2000154149-A/70  
PD 06-JUN-2000  
PF 17-SEP-1999 JP 1999263984

PR NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, WATARU TAKAHASHI, PI KAORI  
NAKAHARA,  
PI SHIN YONEHARA  
PC A61K39/395, A61P29/00, C12N15/09//C07K16/28, C12P21/02, C12N15/00  
CC  
FH Key Location/Qualifiers  
FT CDS (1)..(1764)  
FT mat\_peptide (58)..(1764)  
FT sig\_peptide (1)..(57).  
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location/Qualifiers  
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BASE COUNT 384 a 568 c 485 g 330 t

ORIGIN

Query Match 65.6%; Score 265.8; DB 6; Length 1767;  
Best Local Similarity 78.5%; Pred. No. 7.6e-74;  
Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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QY 181 ggaagcagcctcgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240  
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DB 361 GCTATGACTACTGGGGCCAGGCAACCTGTGACCCGTCTCTCA 405

RESULT 5  
E40700 1768 bp DNA linear PAT 31-JAN-2002  
LOCUS  
DEFINITION Anthuman Fas humanized antibody-containing antirheumatic.  
ACCESSION E40700  
VERSION E40700.1 GI:18627289  
KEYWORDS JP 2000154149-A/71.  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequence.  
1 (bases 1 to 1768)  
AUTHORS Serizawa,N., Haruyama,H., Takahashi,W., Nakahara,K. and Yonehara,S.  
TITLE Anthuman Fas humanized antibody-containing antirheumatic  
JOURNAL Patent: JP 2000154149-A 71 06-JUN-2000;  
SANKYO CO LTD  
OS Artificial Sequence  
PN JP 2000154149-A/71  
PD 06-JUN-2000  
PF 17-SEP-1999 JP 1999263984  
PI NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, WATARU TAKAHASHI, PI KAORI  
NAKAHARA,

[illegible]

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QY	61	gtccagctgtgtgcaatctctgggtctgaagtgtgaagaagcctggtgaagctcagtgaagtgtctc	120
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QY	121	tgcnaagcttcgcgtgtacacatctcaatctgataatgctatacagttggtgtgaagagctctc	180
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QY	181	ggacagggccttgagttgattggaatttaattatctactagataatacaaacatacaac	240
Db	191	GGATGAACCTTGAATGTGGATTGACTTATTAATCCCTTACAAATGGTGTCTCTTACAC	250
QY	241	cagaagcttaaggaggcaagggccacaatgactgtgtagaagaagctgcagcagacagactata	300
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ACCESSION	ARI44016		
VERSION	ARI44016.1		GI:15105883
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 451)		
TITLE	Co./M./Sung.		
JOURNAL	Humanized antibodies reactive with L-selectin		
FEATURES	Patent: US 6210671-A 11 03-APR-2001;		
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Best Local Similarity	77.6%;		Pred. No. 4.8e-70;
Matches 326; Conservative	0; Mismatches 79; Indels 15; Gaps		
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Db	72	GTCCAGCTGTGTGCAATCTCGAAGCTGAGGTGAAGAAACCTGGGAGCTCAGTGAAGGTATCC	131
QY	121	tgcnaagcttcgcgtgtacacatctcaatctgataatgctatacagttggtgtgaagagctctc	180
Db	132	TGCAAGGCTTCTGGATTCACATTCACCTAGCTATGTATGCACTGGGTGAAGAGCACCT	191
QY	181	ggacagggccttgagttgattggaatttaattatctactagataatacaaacatacaac	240
Db	192	GGTCAAGAGACTGTGATGTGATATATTATTTCTTACAAATGATGTATGCAAGTACAT	251
QY	241	cagaagcttaaggaggcaagggccacaatgactgtgtagaagaagcctgcagcagacagactata	300
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Db	371	TATACTATGAGACTATTGGGTCAAGAAACCCGTGTCACCGTCTCTCA	418

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DB	372	GGTAACTAGCTTCGGGTACTTGCATGTCTGGGGCCAAGAAGTACCTGTCACAGCTCTCTCA	431		
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DEFINITION	Drug containing anti-Fas antibody.				
ACCESSION	E40080				
VERSION	E40080.1 GI:18627196				
KEYWORDS	JP 2000I69393-A/77. JP 2000I69393-A/77.				
SOURCE	synthetic construct. artificial sequence. synthetic construct. artificial sequence. 1 (bases 1 to 2071)				
ORGANISM	Serizawa,N., Haruyama,H., Takahashi,W., Yoshida,H., Ichikawa,K., Okuma,T., Otsuki,M., Shiraiishi,A. and Yonehara,S.				
REFERENCE	Drugs Containing Anti-Fas Antibody Patent: JP 2000I69393-A 77 20-JUN-2000; SANKYO CO LTD				
AUTHORS	OS Artificial Sequence PN JP 2000I69393-A/77 PD 20-JUN-2000 PF 30-SEP-1999 JP 1999278301 PR				
TITLE	PI NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, WATARU TAKAHASHI, PI HIROKO YOSHIDA, PI KIMIHISA ICHIKAWA, JUN OKUMA, MASAHICO OTSUKE, AKIO SHIRAIISHI, PI SHIN YONEHARA				
JOURNAL	PC A61P13/12.A61P31/18.A61P37/06.C12N5/10,C12N15/02,C12N15/09, PC A61P9/10, C12P21/08// PC C07K16/28,C12N5/00,C12N15/00,C12N15/00				
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Matches 325; Conservative 0; Mismatches 80; Indels 15; Gaps 1;
QY 1 atgggttggaactgtatcatctcttcttggttaccaagctacaggtgtgactccag 60
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DEFINITION Humanized anti-Fas antibody.
ACCESSION E40911
VERSION E40911.1 GI:18627488
KEYWORDS JP 2000166574-A/100.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2073)
AUTHORS Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
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TITLE Humanized anti-Fas antibody
JOURNAL Patent: JP 2000166574-A 100 20-JUN-2000;
COMMENT SANKYO CO LTD
OS Artificial Sequence
PN JP 2000166574-A/100
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275441
PR NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO TAMAKI
PI C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
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ACCESSION	X65893.S59736			
VERSION	X65893.1	GI:395090		
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SOURCE	human.			
ORGANISM	Homo sapiens			
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AUTHORS	1 (bases 1 to 405)			
TITLE	Schiff,C.			
JOURNAL	Direct Submission			
REFERENCE	Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE			
AUTHORS	2 (bases 1 to 405)			
TITLE	Millil,M., Le Delst,F., de Saint-Basile,G., Fischer,A., Fougereau,M. and Schiff,C.			
REFERENCE	Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire			
JOURNAL	J. Clin. Invest. 91 (4), 1616-1629 (1993)			
MEDLINE	93332287			
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DEFINITION	Humanized anti-Fas antibody.		
ACCESSION	E40912		
VERSION	E40912.1 GI:18627489		
KEYWORDS	JP 2000166574-A/101.		
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	artificial sequence.		
AUTHORS	1 (bases 1 to 2073)		
JOURNAL	Serizawa,N., Haryuyama,H., Nakahara,K. and Tamaki,I. Humanized anti-Fas antibody Patent: JP 2000166574-A 101 20-JUN-2000; SANKYO CO LTD		
COMMENT	OS Artificial Sequence PN JP 2000166574-A/101 PD 20-JUN-2000 PF 29-SEP-1999 JP 1999275441 PR PI NOBUKI SERIZAWA, HIDEYUKI HARYUYAMA, KAORI NAKAHARA, IKUO TAMAKI PC C12N15/09,A61K39/00,A61K39/395,A61P37/02,A61P43/00, PC C07K16/18, PC C12N1/21,C12N5/10,C12P21/08/(C12N1/21,C12R1:19),C12N15/00, PC C12N5/00 CC FH Key Location/Qualifiers FT sig_peptide (23) . (79) FT intron (737) . (1127) FT intron (1173) . (1290) FT intron (1621) . (1717) FT exon1 (23) . (736) FT exon1 (1128) . (1172) FT exon1 (1291) . (1620) FT exon1 (1718) . (2038) FT mat_peptide (80) . (736) FT mat_peptide (1128) . (1172) FT mat_peptide (1291) . (1620) FT mat_peptide (1718) . (2038) FT CDS (23) . (736) FT CDS (1128) . (1172) FT CDS (1291) . (1620) FT CDS (1718) . (2038). FEATURES Source location/Qualifiers 1..2073 /organism="synthetic construct" /db_xref="taxon:32630" BASE COUNT 461 a 686 c 559 g 367 t ORIGIN Query Match   61.8%; Score 250.4; DB 6; Length 2073; Best Local Similarity 77.1%; Pred. No. 6.7e-69; Matches 324; Conservative 0; Mismatches 81; Indels 15; Gaps 1;		
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OY	121	tgcacaagcttcgcgtgtacacattcatgatgtatatacagttggttgagacaagctccct	180
Db	143	TGCAGAAGCTTCGCGGTACACCTTCACACAGCTACGCTAGTGTGAGTACAGAGGCCCTT	202
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DEFINITION Drug containing anti-Fas antibody.  
ACCESSION E40042  
VERSION E40042.1 GI:18627158  
KEYWORDS JP 2000169393-A/39.  
SOURCE JP 2000169393-A/39.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 457)  
AUTHORS Serizawa,N., Haruyama,H., Takahashi,W., Yoshida,H., Ichikawa,K.,  
Okuma,J., Otsuki,M., Shiraiishi,A. and Yonehara,S.  
TITLE Drug containing anti-Fas antibody  
JOURNAL Patent: JP 2000169393-A 39 20-JUN-2000;  
SANKYO CO LTD  
OS Artificial Sequence  
PN JP 2000169393-A/39  
PD 20-JUN-2000  
PE 30-SEP-1999 JP 1999278301  
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PI NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI  
HIROKO YOSHIDA,  
PI KIMIHISA ICHIKAWA,JUN OKUMA,MASAHICO OTSUKI,AKIO SHIRAIISHI, PI  
SHIN YONEHARA  
PC A61K39/395,A61K39/395,A61K39/00,A61P1/16,A61P7/06,A61P9/00, PC  
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10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pin:\*  
16: em\_gss\_vrl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	282	69.6	738	10	BG965088
2	252.2	62.3	633	10	BG961755
3	241.8	59.7	690	10	BG968682
4	238.6	58.9	819	10	BG966397
5	235.4	58.1	770	10	B1249216
6	233.8	57.7	771	10	B140551
7	232	57.3	723	10	BG969577
8	232	57.3	724	10	B1688514
9	230.4	56.9	769	10	B168856
10	226.6	56.0	488	9	AM403591
11	226.6	56.0	764	10	BFS80556
12	226.2	55.9	794	10	BG756463
13	226.2	55.9	840	10	BM007943
14	225.6	55.8	911	10	BE286958
15	225.6	55.7	847	10	B165486
16	224.4	55.7	567	10	BE287568
17	224.2	55.4	739	10	BE284158

18	224.2	55.4	865	10	BG964435
19	224.2	55.4	1093	10	BF974290
20	224	55.3	417	9	AM408371
21	224	55.3	724	10	BG962137
22	223.2	55.1	784	10	BM007990
23	223	55.1	889	10	BF134160
24	222	54.8	598	10	BF104341
25	221.8	54.8	633	10	BG686267
26	221.4	54.7	764	10	BG745457
27	221.2	54.6	1576	11	AK007918
28	221	54.6	896	10	BG963760
29	220.8	54.5	477	10	BF975791
30	220.8	54.5	488	9	AT91363
31	220.8	54.5	494	10	BG60202
32	220.8	54.5	698	10	BF584024
33	220.8	54.5	778	10	BM008290
34	220.8	54.5	849	10	BF582051
35	220.8	54.5	878	10	BG758459
36	220.8	54.5	909	10	BG397239
37	220.8	54.5	1012	10	BF974633
38	220.2	54.4	824	10	BG756421
39	220.2	54.4	904	10	BG758074
40	220.2	54.4	950	10	BF788670
41	220	54.3	513	9	AM402081
42	219.8	54.3	516	9	AM402422
43	219.2	54.1	922	10	BG758876
44	218.8	54.0	477	9	AM408484
45	218.2	53.9	587	9	AM403728

#### ALIGNMENTS

RESULT 1  
LOCUS BG965088 738 bp mRNA linear EST 12-JUN-2001  
DEFINITION 602829160F1 NCL\_CGAP-Co24 Mus musculus cDNA clone IMAGE:4963974 5',  
mRNA sequence.  
ACCESSION BG965088.1 GI:14352725  
VERSION BG965088  
KEYWORDS house mouse.  
SOURCE Mus musculus.  
ORGANISM Mus musculus.  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LHAM10989 row: g column: 15  
High quality sequence step: 716.  
Location/Qualifiers  
1. 738  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4963974"  
/clone\_lib="NCL\_CGAP-Co24"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: colon; Vector: PCMV-SPORE6; Site: 1: NotI;  
Site: 2: SalI; Cloned unidirectionally. Primer: oligo dfr.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCL\_CGAP Library."

#### FEATURES

source  
195 a 186 c 189 g 168 t  
BASE COUNT

## ORIGIN

Query Match 69.6%; Score 282; DB 10; Length 738;

Best Local Similarity 82.1%; Pred. No. 5.7e-76; Matches 340; Conservative 0; Mismatches 65; Indels 9; Gaps 1;

QY 1 atgggttggaacgtatcatcttccttcgtgtaccacagctcaaggtgtgcaactccag 60  
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Db 40 ATGGGTAGAGAGCTGTATCATCTTCTTCTGTAGCAACAGCTTACAGGTGTACCTCCAG 99  
QY 61 gtccaagcttggtgagcttggtgagtgaaagagctggaagctgaagtgagtc 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 100 GTCCAGCTGCAGAGCTGTGGCTGTAGAGCTGTAGAGCTGTGGCTGTAGAGATCTCC 159  
QY 121 tgaagaagcttcggtacacaaatcactgatatgatacaagtggtgagagctcc 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 160 TGCAGAGGTCGCGTACACATTCAGATTATCTATACATGTGGGTGAAGCAGAGTCAT 219  
QY 181 ggaacagagctcgagtgagtgagtgatattatattacatgataataacaatacaac 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 220 GCAAGAGCTGTAGAGTGAGTGTGAGTATTAATCTTACTATGTAACAACTGCAAC 279  
QY 241 cagaagtttaaggcgaagccacaatgactgtagacaagtcgaagcagacagctata 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 280 CAGAAAGTTGAGGCAAGGCAACATGACTGTAGACAAATCTCCGCGACAGCTATATG 339  
QY 301 gaactagctcttgagatctgaggtacgagcttattactgtggaaga----- 351  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 340 GAACCTTGCCAGATTGACAGCTGTAGAGATTCTGCATCTATTACTGTGCAAGATTATTCGG 399  
QY 352 gcgcctcgatataggactactggtggtcaagagtcacctgtcacgcgtccctca 405  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 400 GGAACGTATGCTGTGAGCTACTGGGTGCAAGAACTCAGTCAACCGTCTCTCTCA 453

## RESULT 2

BG961755

LOCUS 602826375F1 NCI\_CGAP\_Co24 Mus musculus cdna clone IMAGE:4981242 5',

DEFINITION mRNA sequence.

ACCESSION BG961755

VERSION BG961755.1 GI:14349392

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 633)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabrs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.jnl.gov

Plate: LLM10982 row: e column: 19

High quality sequence stop: 617.

Location/Qualifiers

1. 633

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone\_lib="IMAGE:4981242"

/clone="NCI\_CGAP\_Co24"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; NotI:  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

## BASE COUNT

Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

160 a 153 c 163 g 157 t

## ORIGIN

Query Match 62.3%; Score 252.2; DB 10; Length 633;

Best Local Similarity 83.7%; Pred. No. 8.3e-67; Matches 309; Conservative 0; Mismatches 58; Indels 2; Gaps 2;

QY 1 atgggttggaacgtatcatcttccttcgtgtacc-acaagctcaaggtgtgcaactcc 59  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 40 ATGGGTAGAGAGCTGTATCATCTTCTTCTGTAGCAACAGCTTACAGGTGTACCTCCCA 99  
QY 60 gtccaagcttggtgagcttggtgagtgaaagagctggaagctgaagtgagtc 119  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 100 GTCCAGCTGCAGAGCTGTGGCTGTAGAGCTGTAGAGCTGTGGCTGTAGAGATTTTC 159  
QY 120 ctgcaagcttcggtacacaaatcactgatatgatacaagtggtgagagagctcc 179  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 160 CTGCAAGGTTCCGCTACACATTCAGATTATGCTTTACACTGGGTGAAGCAGAGTCA 219  
QY 180 tgaacagagctcgagtgaga-tggagttatataattactatgataaacaactaca 238  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 220 TGCAGAGGTCGCGTACAGATTATCTTACTATGTAACAACTGCAACAGCTTACA 279  
QY 239 accagaagtttaaggcgaagccacaatgactgtagacaagtcgaagcagacagctata 298  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 280 ATGAGAGGTTTAAAGCGCAAGGCCCAATGACTGTAGCAACATCTCCAGCAGACCTATA 339  
QY 299 tgaactagctcttgagatctgagatacagcgcttattactgtgcaagagcgct 358  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 340 TGCAGGTTGCCAGATTGACATCTGAGGATCTGCATCTATTATTGTGCAAGAGGGAAG 399  
QY 359 ggtatagtg 367  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 400 CGTATGGGG 408

## RESULT 3

BG968682

LOCUS 602836513F1 NCI\_CGAP\_Co24 Mus musculus cdna clone IMAGE:4990947 5',

DEFINITION mRNA sequence.

ACCESSION BG968682

VERSION BG968682.1 GI:14356306

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 690)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabrs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.jnl.gov

Plate: LLM1007 row: j column: 04

High quality sequence stop: 679.

Location/Qualifiers

1. 690

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone\_lib="IMAGE:4990947"

/clone="NCI\_CGAP\_Co24"

/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: PCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 173 a 192 c 170 g 155 t  
ORIGIN

Query Match 59.7%; Score 241.8; DB 10; Length 690;  
Best Local Similarity 76.2%; Pred. No. 1.4e-63;  
Matches 313; Conservative 0; Mismatches 92; Indels 6; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgtgtacacagctacaggtgtgactccag 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 34 ATGGATGGAGCTGTATCATCTCTCTGTGTACACAGCTACAGGTCTCCACG 93  
gtccagctgtgacgtctggagctgaagctgtgagctgaagctgaagctgtgac 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 94 GTCCAACTGCAGCAGCTGGGGCTGACCTGGTGAAGCTTGAGCTTCAAGTTGTCC 153  
121 tgcgaagcttcgagctacacattcactgatatgtatacagtggtgagagagctcct 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 154 TGCAGAGCTTCTGCTACCTTACCACTGATGACCTGGGTGAAGAGAGGCTT 213  
181 ggacagagctcgtgagtgatgtgagttataattactgtataataacactaac 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 214 GGACAAAGCCTTGATGATGGAAATATTAACTATATGATGATGATGATGATGAT 273  
QY 241 cagaagtttaaggcgaagccacaaatgactgtagaagaagctgaagagagagcctata 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 274 GAGAAAGTTCAAGACCAAGCCACATTGACTGTATGATCACTCCAGACAGCCCTACATG 333  
QY 301 gaacttagtcttctgagatctgagatacagccgtttactgtgcaagagcg----- 354  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 334 CAGCTCAGACAGCTCAGATCTGGCGACTGCGGCTATATGCTGATCAATAAGTTGTCTA 393  
QY 355 gccctgatatgactactcgtgggtcaaggtacacctgtcaacctctca 405  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 394 CGTTATTCTATGACTGATGGGGTCAAGAACCTCAGTCAAGCTCTCTCTCA 444

RESULT 4 819 bp mRNA linear EST 12-JUN-2001  
LOCUS BG966397  
DEFINITION 602832896F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4987631 5',  
mRNA sequence.  
ACCESSION BG966397  
VERSION BG966397.1 GI:14354034  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 819)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LHAM10998 row: O column: 24  
High quality sequence stop: 766.  
Location/Qualifiers  
1. 819  
/organism="Mus musculus"  
/strain="FVB/N"

/db\_xref="taxon:10090"  
/clone="IMAGE:4987631"  
/clone\_id="NCI\_CGAP\_Co24"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: PCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 206 a 229 c 199 g 185 t  
ORIGIN

Query Match 58.9%; Score 238.6; DB 10; Length 819;  
Best Local Similarity 75.7%; Pred. No. 1.5e-62;  
Matches 311; Conservative 0; Mismatches 94; Indels 6; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgtgtacacagctacaggtgtgactccag 60  
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Db 25 ATGGATGGAGCTGTATCATCTCTCTTTTGTGTACCAAGCTACAGGTCTCCACG 84  
gtccagctgtgacgtctggagctgaagctgtgagctgtgagctgtgagctgtgac 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 85 GTCCAACTGCAGCAGCTGGGGCTGACCTGGTGAAGCTTGAGCTTCAAGTTGTCC 144  
121 tgcgaagcttcgagctacacattcactgatatgtatacagtggtgagagagctcct 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 145 TGCAGAGCTTCTGCTACCTTACCACTGATGATGATGATGATGATGATGATGATGAT 204  
QY 181 ggacagagctcgtgagtgatgtgagttataattactgtataataacactaac 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 205 GCACAGGCTTGTGATGGATGGAGGATTTATCTTACCAATGGTGCACATTAATTTTAT 264  
QY 241 cagaagtttaaggcgaagccacaaatgactgtagaagaagctgaagagagcctata 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 265 GAGAAAGTTCAAGACCAAGCCACACTGACTGTAGCAATCCTCCAGACAGCCACATG 324  
QY 301 gaacttagtcttctgagatctgagatacagccgtttactgtgcaagagcg----- 354  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 325 CAACTCAGCAGCTCAGATCTGGAGGACCTGCGGCTATATGATGATGATGATGATGAT 384  
QY 355 gccctgatatgactactcgtgggtcaaggtacacctgtcaacctctca 405  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 385 TTTCATGCTATGACTGATGGGGTCAAGAACCTCAGTCAAGCTCTCTCTCA 435

RESULT 5 770 bp mRNA linear EST 17-JUL-2001  
LOCUS B1249216  
DEFINITION 602994779F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:5150778 5',  
mRNA sequence.  
ACCESSION B1249216  
VERSION B1249216.1 GI:14796364  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 770)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LHAM1372 row: m column: 19  
High quality sequence start: 4  
High quality sequence stop: 769.

FEATURES  
source  
Location/Qualifiers  
1. 770  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone\_image="5150778"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-Sport6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lohar Hennishausen/Robin Humphreys, NIH"

BASE COUNT 188 a 216 c 193 g 173 t

ORIGIN

Query Match 58.1%; Score 235.4; DB 10; Length 770;  
Best Local Similarity 75.2%; Pred. No. 1.4e-61;  
Matches 309; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 1 atgggttggaactgtatcatctcttcttctgttccacagctaaagtggtcactccag 60  
DB 35 ATGGGATGGAGCTCTATCATCTCTCTGTGTACCAACAGCTACAGGTCTCCAG 94  
QY 61 gtccagctgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 120  
DB 95 GTCCAACTGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 154  
QY 121 tgcgaagcttcgagctacacattcattatgctatcaagtggtgagacagctcct 180  
DB 155 TGCAAGGCTTCTGCTACCTTCCACAGCTACGATGATACCTGGCGAGACAGGCTT 214  
QY 181 ggaagagcttcgagctgagctgagctgagctgagctgagctgagctgagctgagct 240  
DB 215 GGACAGGCTTGTAGTGTGATGAGAGATTCATCTTAATGATGATTAATCTTAATCT 274  
QY 241 cagaagtttaaggcaagccacaaatgactgtagacaaagctgagacagacagctatag 300  
DB 275 GAGAAAGTTCAGAGGCGCAAGGCGCAAGCTGATGACACATCTCCAGACAGCTAGCTG 334  
QY 301 gaacttgcttcttgagatctgagatagacagcgcttattactctgtgcaagagcg 355  
DB 335 GATCTCAGCAGCCTGATCATCTGAGAGCTCTGCGCTCTATTACTGTGCAAGGCGACTAT 394  
QY 356 -ccgtgatatgagctgagctgagctgagctgagctgagctgagctgagctgagct 405  
DB 395 AGCTGATCTTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 445

RESULT 6  
BF140551 771 bp mRNA linear EST 24-OCT-2000  
LOCUS 601787584F1 NCI\_CGAP\_Lu30 Mus musculus cDNA clone IMAGE:4015172 5',  
DEFINITION mRNA sequence.  
ACCESSION BF140551  
VERSION BF140551.1 GI:10979591  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 771)  
NIH-MGC http://mgc.nci.nih.gov/  
Contact: Robert Strausberg, Ph.D.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
COMMENT

FEATURES  
source  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
http://image.lnl.gov  
Plate: LHAM260 row: h column: 21  
High quality sequence stop: 648.  
Location/Qualifiers  
1. 771  
/organism="Mus musculus"  
/strain="C2EHC II"  
/db\_xref="taxon:10090"  
/clone\_image="4015172"  
/clone\_lib="NCI\_CGAP\_Lu30"  
/tissue\_type="tumor, metastatic to mammary"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: SalI; transgenic model MMTV-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 179 a 215 c 195 g 182 t

ORIGIN

Query Match 57.7%; Score 233.8; DB 10; Length 771;  
Best Local Similarity 73.6%; Pred. No. 4.3e-61;  
Matches 298; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctcttcttctgttccacagctaaagtggtcactccag 60  
DB 15 ATGGGATGGAGCTCTATCATCTCTCTGTGTACCAACAGCTACAGGTCTCCAG 74  
QY 61 gtccagctgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 120  
DB 75 GTCCAACTGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 134  
QY 121 tgcgaagcttcgagctacacattcattatgctatcaagtggtgagacagctcct 180  
DB 135 TGCAAGGCTTCTGCTACCTTCCACAGCTACGATGATACCTGGCGAGACAGGCTT 194  
QY 181 ggaagagcttcgagctgagctgagctgagctgagctgagctgagctgagctgagct 240  
DB 195 GGACAGGCTTGTAGTGTGATGAGAGATTCATCTTAATGATGATTAATCTTAATCT 254  
QY 241 cagaagtttaaggcaagccacaaatgactgtagacaaagctgagacagacagctatag 300  
DB 255 GAGAAAGTTCAGAGGCGCAAGGCGCAAGCTGATGACACATCTCCAGACAGCTAGCTG 314  
QY 301 gaacttgcttcttgagatctgagatagacagcgcttattactctgtgcaagagcg 360  
DB 315 GAGCTCAGCAGCCTGATCATCTGAGAGCTCTGCGCTCTATTACTGTGCAAGGCGTACTAC 374  
QY 361 tatatgactacttgagctgagctgagctgagctgagctgagctgagctgagctgagct 405  
DB 375 GTATTGACTACTGTGGGCCAAGGCCACCATATCATAGTCTCTCA 419

RESULT 7  
BG969577 723 bp mRNA linear EST 12-JUN-2001  
LOCUS 602837386F1 NCI\_CGAP\_K1d14 Mus musculus cDNA clone IMAGE:4971813  
DEFINITION 5', mRNA sequence.  
ACCESSION BG969577  
VERSION BG969577.1 GI:14357214  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 723)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
COMMENT

COMMENT	FEATURES	BASE COUNT	ORIGIN
Contact: Robert Strausberg, Ph.D. Email: cgapb-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.lnl.nh.gov">http://image.lnl.nh.gov</a> Plate: LHAM10957 row: 1 column: 22 High quality sequence status: 723.	source location/Qualifiers 1. 723 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4971813" /clone_id="NCI CGAP Kid14" /lab_host="DH10B (TI phage-resistant)" /note="Organ: kidney; Vector: pCMV-Sport6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library.  "	179 a 196 c 193 g 155 t	
Query Match Best Local Similarity 57.3%; Score 232; DB 10; Length 723; Matches 305; Conservative 0; Mismatches 100; Indels 3; Gaps 1;			
QY 1 atgggttggaactgtatcatctcttcttggttaccacagcaagtggtgcatcccaag 60 Db 19 ATGGGATGGACCTCTATCATCTCTTCTTGGTAGCAGACAGCTACAGGTCCACG 78			
QY 61 gtccagcgtggtcagctcgtgggctgtaggttgaaagacccctgagctcagtgagttcc 120 Db 79 GTCCAACTGCAGCAGCCCTGGGTCTGTGTGTGGTAGAGCCCTGGAGCTTCAGTGAAGCTGTCC 138			
QY 121 tgcgaagcttcgggctcaacattcaactatattgctatcacagtggtgtagaaggctctc 180 Db 139 TGCAGGCTTCTGGCTACACATTCACAGCTACAGCTGAGTGCAGTGGTGTAAGCAGAGGCT 198			
QY 181 ggcaaggcctcgtggtgattgtagattatattactatgatataataacaactaac 240 Db 199 GGACAAAGCCCTTGATGGATTTGAGAGATTTATCTCTAATAGGTGAGGACTAATCAAT 258			
QY 241 cagaagtttaaggccaaggccacaatgactcttagcaagtcgagagacagccatattg 300 Db 259 GAGAAATTCAAGGGGAAAGGCCACACTGACTGAGACAAATCTCCAGACACAGCTACGCG 318			
QY 301 gaacttagttcttgagactctgagatatacgccgttatactactgtgcaa--gaagcgcc 357 Db 319 GATCTCACACAGCCGACATCTGAGAGACCTCTCGGCTCTTTACTGTGCAAGAGAGAGGCCCC 378			
QY 358 tggatataagactactcgtgggtcaaggtacccctgtcacgcgtctccca 405 Db 379 AAAGGTTTGCTTACTCTGGGCCAAAGGAGACTGTGCTACCTGTCTTGCA 426			
RESULT 8			
LOCUS BFL68514 724 bp mRNA linear EST 30-OCT-2000			
DEFINITION 60177541F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017075 5',			
ACCESSION BFL68514			
VERSION BFL68514.1 GI:11048866			
KEYWORDS EST.			
SOURCE house mouse.			
ORGANISM Mus musculus			
REFERENCE Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

FEATURES	BASE COUNT
source	ORIGIN
<p>           NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>.            National Institutes of Health, Mammalian Gene Collection (MGC)            Unpublished (1999)            Contact: Robert Strausberg, Ph.D.            Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>            Tissue Procurement: Gilbert Smith, Ph.D.            cDNA Library Preparation: Life Technologies, Inc.            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)            DNA Sequencing by: Incyte Genomics, Inc.            Clone distribution: MGC clone distribution information can be            found through the I.M.A.G.E. Consortium/LML at:  <a href="http://image.lnl.gov">http://image.lnl.gov</a>            plate: LLM9265 row: h column: 04            High quality sequence stop: 61.            Location/Qualifiers            1..724            /organism="Mus musculus"            /strain="C57BL/6J (f1)"            /db_xref="taxon:10090"            /clone IMAGE:4017075"            /clone_lib="NCI CGAP Lu29"            /tissue_type="spontaneous tumor, metastatic to mammary.            Stem cell origin."            /lab_host="DH10B"            /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;            Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.            Library constructed by Life Technologies. Investigator            providing samples: Gilbert Smith, NIH"         </p>	<p>           185 a 186 c 194 g 159 t         </p>

Query Match	57.3%	Score 232	DB 10	Length 724
Best Local Similarity	74.8%	Pred. No. 1,5e+60		
Matches 305	Conservative 0	Mismatches 100	Indels 3	Gaps 1
QY	1	atgggttggaactgtatcatcctctctctgtgttaccacagctacagatgtgtgcactccag	60	
Db	38	atggatgagactggatctttatttttaacctgtcagtaactacagctgctccactctgag	97	
QY	61	gtccagctcgtgtgcnctctgggggttaagttgaagaagcctgtgaagtcagtgaaagtgc	120	
Db	98	gtccgcctgcacgacactgttgagacttaagctgtgaagcctggggcttgcagtgaagtatcc	157	
QY	121	tgcgaagcttcocggtctaacacatcttcaactgtatattgtctatacagttggtgacagctcct	180	
Db	158	tgcgaagcttctggtgttactcaattcacttgcgtactcactatgacactgtggaagaaagtctt	217	
QY	181	gtacagggcctcagtgatgtgagttatlaattactatgataataacaaactacaac	240	
Db	218	gaaaagacccttgatggattggagagatttaaccttacacactgctggtgactccttaaac	277	
QY	241	cagaagtttaagggaagggccaaatgtactgtgaagcaagtcgacagacagccctatgt	300	
Db	278	cagaaggttcaaggggcgaagccacattgtactgtagacaaatcctccagacacaccttaacg	337	
QY	301	gaacttaqctctctagaatcttgagatcacggcgttttaactgtgcgaaga---gcggcc	357	
Db	338	cagctcaagagcgtcactacatcttgagacactctgcagctcttttactgtgcaagaagctatc	397	
QY	358	tgttatatgactactagggtgtcaaggtacacctgtgcaacctctcctca	405	
Db	398	aggcctataggactactactgggggtcgaagaaacctgacacacgctcctca	445	

RESULT 9

BF168856

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

BF168856

6017731.f1

NCI\_CGAP\_lu29

Mus musculus

cDNA clone IMAGE:4017147

5'

769 bp

mRNA

linear

EST 30-OCT-2000

BF168856

GI:11049208

EST.

SOURCE	house mouse.
ORGANISM	Mus musculus.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	Nih-Mgc http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strussberg, Ph.D. Email: cga@bs-remail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLNMG965 row: k column: 04 High quality sequence stop: 678. Location/Qualifiers 1..769
FEATURES	/organism="Mus musculus" /strain="CZECH II (fetal)" /db_xref="taxon:10090" /clone="IMAGE:4017147" /clone_lib="NCI CGAP_Lu29" /tissue_type="spontaneous tumor, metastatic to mammary." stem_cell_origin="" /lab_host="DH10B" /note="Organ: lung; Vector: pCMV-SPORE6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT	190 a 226 c 189 g 164 t
ORIGIN	
Query Match	56.9%; Score 230.4; DB 10; Length 769;
Best Local Similarity	74.5%; Pred. No. 4.8e-60;
Matches 304:	Conservative 0; Mismatches 101; Indels 3; Gaps 1;
OY	1 atgggttggaactgatatcatcttccttcgtgtaccacagatgtgcaactccag 60
Db	42 ATGGGATGTGAGCTGATCTTTATTATTCCCTGTCAAGTAACAGTGTCACACTGAG 101
OY	61 gtccagctgtgtcagttcttggggtcgaggtagaaacctggaagtccaagtgtc 120
Db	102 GTCCAGCTGTGACACCTCTGGACCTGAGCGTGGGAAGCGCTGCCGTTCAGTGAAGATATCC 161
OY	121 tgcaaatcttcgggtgtacaattcatactgatatttgtatatacagttgggtagaagactct 180
Db	162 TGCAAGGCTTCTGGTACTCATCTTCCTGCTACTGTACTGATGGGTGAGAAGAACTCTT 221
OY	181 ggacagggcctcagatgtgatttgagatttaataattactatgataataaacatacaac 240
Db	222 GAAGAAGACCTTGATGATGTGAGAGATTAATTAATCTTAGACACTGGTGTACTACTAACAAC 281
OY	241 cagaagttaaagggaagccacaatgactgtgaagcaagtcgaagagacagaccatata 300
Db	282 CAGAAGTTCAGAGGGCAAGGCCACATTTGACTGTAGAACAAATCTCCAGCACACCCTACAG 341
OY	301 gaacttagttctttaagatctcagatatacggcggttatctaactgtgcaaga--gcggcc 357
Db	342 CAGCTCAAGAGCGCTGACATCTGAGAGACTCTGAGAGCTATTACTGTGCCAAGAAGCTACATC 401
OY	358 ttgattatggaactacttgggttcaagtaacctgtgccacgcttcctca 405
Db	402 AGGCGTTAGGACTACTCGGTCACGAAGAACCTGACGACCGTCTCTCA 449
RESULT 10	
AW403591	488 bp mRNA linear EST 16-FEB-2000
LOCUS	AW403591

DEFINITION	UI-HF-BK0-abo-b-01-0-ui.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3056184 5', mRNA sequence.					
ACCESSION	AM403591					
VERSION	AM403591.1 GI:6922577					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 488) NIH-MGC http://mgc.ncl.nih.gov/. National Institutes of Health. Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: rgs@bbs-riemail.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://www.bio.lnl.ni.gov/bbrp/image/image.html">www-bio.lnl.ni.gov/bbrp/image/image.html</a> Seq primer: M13 Forward					
FEATURES	Location/Qualifiers 1..488 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3056184" /clone_lib="NIH_MGC_36" /tissue_type="lymph" /cell_type="germlinal center B cells" /cell_line="MGC85" /lab_host="DH10B (LTI)" /note="Vector: pRT73-Pac; Site_1: NotI; Site_2: Eco RI; constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). directionally cloned Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."					
BASE COUNT	111 a 136 c 140 g 101 t					
ORIGIN						
Query Match	56.0%; Score 226.6; DB: 9; Length 488;					
Best Local Similarity	73.5%; Pred. No. 5.8e-59;					
Matches 311:	Conservative 0; Mismatches 94; Indels 18; Gaps 1;					
1	atcggttggaactgatacatcttccttccttcggtgtaaccagctacagggtgtgcactccag	60				
2	acgaggtgacctggagagatcctctttttggggcagacgccacaagtgcccactccacg	61				
61	gtccagctggtgtagctctggtggctgaagtgaagaagctctggagctcagtgaaaggtgcc	120				
62	gtccagcttggtagaacatctggggctcaggggaagagccctggggccctcagtgaaaggtgcc	121				
121	tgcagaagcttcgggttacatcacatcactgatattgctatacagtggtgtagacaggtcct	180				
122	tgcagaagcttcttgcatcacccttccactaatctgtctatatcattgggtggcgcagcccc	181				
181	ggacagggccttcgagattggaattgagatttaatacttatcattgataataacaatacaac	240				
182	ggacaaaagccttgatgtgatggagatgagatcaacgcctggccaataatgtaaacaaaatattcca	241				
241	cagaagctttaagggcaagggcccaatgactgtatagcagaagtcgacagacagcctatatg	300				
242	cagaagcttccagggcagagatccactttccacagggacacatccgcagacacacccctacattg	301				
301	gaactagttctcttgagatctgagataacagcgcgtttattactgtgcaagaagc-----	354				
302	gagctgacagcctcagatctgaacacacagcgcgtgtctatctgtgcgacagccgagaat	361				
355	-----gctgtgatatggaactactggtggctaaaggtaaccttgtcacggtctcc	402				

DB	364	TACTATGGTTCAGGGAGTTCCTCTTACTACTACTGGGGCCAGGAGAACCCCTGGTACCGCTTCC	421
OY	403	tca 405	111
Db	422	TCA 424	111
RESULT	11		
LOCUS	BF580556		
DEFINITION	602097359P1 NCI_CGAP_Co24 Mus musculus CDNA clone IMAGE:4217102 5',	764 bp	linear
ACCESSION	BF580556		
VERSION	BF580556.1	GI:11654268	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 764)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Jeffrey E. Green, M.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMN at:		
	http://image.lnl.gov		
	Plate: L1AM9795	row: f	column: 15
	High quality sequence stop: 694.		
FEATURES	Location/Qualifiers		
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	/clone_lib="NCI CGAP Co24"		
	/lab_host="DH10B (TI phage-resistant)"		
	/note="Organ: colon; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."		
BASE COUNT	194 a	198 c	195 g
ORIGIN			177 t
Query Match	56.0%;	Score 226.6;	DB 10; Length 764;
Best Local Similarity	74.1%;	Pred. No. 7.1e-59;	
Matches 300;	Conservative 0;	Mismatches 104;	Indels 1; Gaps 1;
OY	1	atgggttggaactgtatcatcttcttcttggttaccacaagctacaggtgtgcatcccaag	60
Db	37	ATGGGATGGAGCTCATATCTCTCTTGGTAGCAACAGCTACAGGCTCCACTCCAG	96
OY	61	gtccagcgtgtgtgcaactctggggcttaggttgaaagaaagctggagagtcagtaagtg	120
Db	97	GTTCAACTGTCACACACCCTGGGGTCTGTGGCTGGAGGCGCTGGAGCTTCAGTGAAGCTGTCC	156
OY	121	tgcagaagcttcoggtacacacatcctactgattatgctatacagttgggtgagacaagctcct	180
Db	157	TGCAAGGCTTCTGGCTTACACATTTCACGAGCTACCTGGATGCACTGGGTGAGCAGAGGCT	216
OY	181	ggacagggcctcagatggatggagttatataattctatagataataacaaacacaaac	240
Db	217	GGACCAAGGCTTGAATGGA-TGGAGAGAGATTATCTTACTAGTGTGGCAGGACCAACTACAT	275
OY	241	cagaagtttaaggggaaagggcacaatgagctctgagacaagtcgagagacagccatata	300
Db	276	GAGAGCTTCAGAGGGGCAAGGCCACACTGACTGATGAGACACATCTCCAGCAGACCCATACGG	335

QY	301	gaactagttctcttgaagatctggaagatacggccgttattactctgcaagagcgcttg	360
DB	336	GATTTTCACGAGCCTTACATCTGAGGACCTCAGGGGCTCTATTATGTACAAAGAGAGGGGAAA	395
QY	361	tatatgaagactagggtcgaagatcccttgcacgcgtctctca	405
DB	396	GAGTTTGACTACTGGGGCCCAAGGACCACTCTCATATGTCCTCA	440
RESULT 12			
LOCUS	BC756463	794 bp	MRNA
DEFINITION	60271579551 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855894 5',		
ACCESSION	BC756463		
VERSION	BC756463.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	NIH-MGC http://mhc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@bbs-remail.nih.gov		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.lnl.gov		
	Plate: L10M1705 row: n column: 23		
FEATURES	High quality sequence stop: 774.		
SOURCE	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:4855894"		
	/clone_1db="NIH_MGC_48"		
	/tissue_type="Primary B-cells from tonsils (cell line)"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;		
	Site_2: EcoRI; cDNA made by oligo-dT priming.		
	Directionally cloned into EcoRI/XhoI sites using the		
	following 5' adaptor: GGGACGAG(G). Size-selected >500bp		
	for average insert size 1.8kb. Library constructed by Ling		
	Hong in the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies).		
	Note: this is a NIH-MGC Library."		
BASE COUNT	173 a 253 c 219 g 149 t		
ORIGIN			
Query Match	55.9%; Score 226.2; DB 10; Length 794;		
Best Local Similarity	73.6%; Pred. No. 9.6e-59;		
Matches 307; Conservative	0; Mismatches 98; Indels 12; Gaps 1;		
QY	1	atgggttggaactgtatcatctcttcttggttacacagctacagtggtgcacccag	60
DB	47	ATGGACTGGACCTGGAGGATCCTCTTCTTGGTGGCAGACGACCAAGGCCACATCCAG	106
QY	61	gtccacgtcgtgacgtctcgtgggctgtaggaagcctcgtggagctcagtgaaagtgctc	120
DB	107	GTGCACCTGTCGTCAGTCGTGGGGCTGAAGAGCCTGGGGCCTCAGTGAAGGTCTCC	166
QY	121	tgcgaagcttcgcgtgtacacattcactgatatgtatacagtggtgtgaagacgctct	180
DB	167	TGCAGGCGTTCTGGATTACCTTCACCGCGTAATATATGCACTGGGTCGACAGGCCCT	226



0y	181	ggaacggggccctcggatggaattggaggtttatattatctatattctatgataatacaaacacacac	240
Db	227	ggacacagggcttggattgattggatggatgacacacccctaacagaggggccacaaactatgtca	286
0y	241	cagaagttcaaggaggaagggccacaatgactgtlagaacaagtcgaacgacagacagccataatg	300
Db	287	cagaagtttcaagggcaggggtcacacattgacacagggagacagctgcacagcagacagccatcatg	346
0y	301	gaacttattctttagatattctgtgagataagcgccgtttatctatctgtgaagagc-----	353
Db	347	gagctgacacagcagcctgacatctgacgacacacggccggctgtttactgtgccaagtccttgagc	406
0y	354	-----ggccctgatatagactactcgggtgtaaggtacccttgcacgtctcccca	405
Db	407	agtgccctggtacacatttgcacttactggggccacaggaacccctggtatccgttccttca	463
RESULT 13			
LOCUS BM007943 840 bp mRNA linear EST 30-OCT-2001			
DEFINITION 60361765F01 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450416 5',			
mRNA sequence.			
ACCESSION BM007943			
VERSION BM007943.1 GI:16522297			
KEYWORDS EST.			
SOURCE human.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE 1 (bases 1 to 840)			
AUTHORS NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Robert Strausberg, Ph.D.			
Email: <a href="mailto:cgabes@email.nih.gov">cgabes@email.nih.gov</a>			
Tissue Procurement: Dr. Mark Watson			
CDNA Library Preparation: Ling Hong/Rubin Laboratory			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LML at:			
<a href="http://image.llnl.gov">http://image.llnl.gov</a>			
plate: LCM1939 row: b column: 17			
High quality sequence stop: 831.			
FEATURES			
Source Location/Qualifiers			
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EcoRI; CDNA made by oligo-dT priming. Directionally cloned			
into EcoRI/XhoI sites using the following 5' adaptor:			
GGCGACGAG(G). Library constructed by Ling Hong in the			
Laboratory of Gerald M. Rubin (University of California,			
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and			
Superscript II RT (Life Technologies). Note: this is a			
NIH_MGC Library."			
BASE COUNT 191 a 258 c 228 g 163 t			
ORIGIN			
Query Match 55.9%; Score 226.2; DB 10; Length 840;			
Best Local Similarity 73.6%; Pred. No. 9.9e-59;			
Matches 307; Conservative 0; Mismatches 98; Indels 12; Gaps 1;			
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0y	61	gttcgagccggtgcagctctcggggtctgagtggaagccttggaagctcagtgaaagtgctc	120

Db	99	GTCCAGCTGTGTGTCACATCTGTGAGAACATGAGTGAAGAACCTGGGGCCTCAGTGAAGTCTTCC	158
Qy	121	tgcaaacctccgcgtctcaacatctcaatctatctgctatacagctgggtgagacagctcct	180
Db	159	TGCAAGGCGCTTGTGTGTACACCTTTTACCAAGCTATGTGTATCAACTGGGTGCGACAGGCCCT	218
Qy	181	ggacaggccctcagctgagcttgatctgagttatctaatctactatgataatcaaacctaac	240
Db	219	GGACAGACGGGCTTGATGTGATGTGGATGGATGATACCGGCTTACATGTGTGACACAAATATGCA	278
Qy	241	cagaagcttaagggcagaagcccaatgactctgagacaagctcagcagacagcctata	300
Db	279	CAGAGATGCCAGGCGAGAGTACCATGTGATGATCAGACACATCGACGAAACGTCTATATG	338
Qy	301	gaactagtctcttgatgacttgagatacagcgcttattctctgcaagagcgccctgg	360
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DEFINITION	60109247091 NCI_CGAP_Mam5 musculus cdna clone IMAGE:3487241 5',		
ACCESSION	BE286958		
VERSION	BE286958.1		
KEYWORDS	GI:9165654		
SOURCE	EST.		
ORGANISM	house mouse.		
	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 911)		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a> Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLM8524 row: k column: 18 High quality sequence stop: 688. Location/Qualifiers 1. 911		
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	/note="Organ: mammary; Vector: PCMV-SPORT6; Site1: SalI; Site2: NotI; Cloned unidirectionally. Primer: oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"		
BASE COUNT	190 a 262 c 261 g 197 t	1	others
ORIGIN			
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Best Local Similarity	75.2%;	Prod. No. 1.2e-58;	
Matches 310;	Conservative 0;	Mismatches 95;	Indels 7; Gaps 2;



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QY 1 atgggttggaaactgtatcatcttcttcttggttaccacagctaacagtgctgccag 60
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QY 121 tgcacagcttcgcgctacacattcactcattatgctatagtggtg-agaagagctcc 179
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QY 180 tggacagggcctcagatggaattggaatttaataattactatgataataacataca 239
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DEFINITION 60177393F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4019039 5',
            mRNA sequence.
ACCESSION  BF165486
VERSION     BF165486.1 GI:11045851
KEYWORDS   EST.
SOURCE      house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 847)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHAM270 row: 1 column: 24
            High quality sequence stop: 760.
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    Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
    Library constructed by Life Technologies. Investigator
    providing samples: Gilbert Smith, NIH"
BASE COUNT  179 a      223 c      242 g      203 t
ORIGIN

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Query Match      55.7%; Score 225.6; DB 10; Length 847;
Best Local Similarity 73.8%; Pred. No. 1.5e-58;
Matches 301; Conservative 0; Mismatches 104; Indels 3; Gaps 1;

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Db 14 ATGGGATGGAGCTGTATCATCTCTCTTGCGACGACACAGCTACAGGTCCTCCAG 73
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QY 181 tggacagggcctcagatggaattggaatttaataattactatgataataacataca 240
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QY 241 ccgaaatttaaggaggaagcccaaatgactgtagacaagctgcaagagcaagctatatg 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 254 TGAAGATTCAGAGAGAGAGGCGCACCTGACTGTAGACAAACCTCCACAGAGCCTACATG 313
QY 301 ggaacttagtcttcttgagatctgagatacagccgttatactgtgcaagaagcgccctg 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 314 GAGCTCAGCAGCCTGTGACATCTGTGAGACTCTGGGCTCTACTGTACAAAGAGGACTACAGT 373
QY 361 tata---tgaactactcgggggtcaaggtaccctgtgtaacgctccctca 405
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Db 374 GTTACCTTGTGACTGTGAGGCGCAAGGACACACTATCACAGTCTCTCA 421

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Search completed: August 26, 2002, 16:13:39  
 Job time: 4333 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 15:05:06 ; Search time 266.46 Seconds  
(without alignments)  
2609.586 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405  
Sequence: 1 atgggttgacgtatcatc.....ccctgtcaccctctcctca 405

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	ID
1	405	100.0	405 21 AAAS9694
2	334.6	82.6	405 21 AAAS9692
3	277.2	68.4	524 12 AAQ14802
4	272.2	67.2	446 11 AAQ014652
5	265.8	65.6	1767 19 AAV61363
6	265.8	65.6	1767 21 AAA78271
7	265.8	65.6	1768 19 AAV61364
8	265.8	65.6	1768 21 AAA78272
9	265.8	65.6	1768 21 AAA78272

10	254.4	62.8	424	17	AA742717	HuK3 VH coding se
11	253.6	62.6	451	15	AAQ6702	DREB-200 Humanised
12	253.6	62.6	2071	19	AA70080	Anti-Fas humanised
13	253.6	62.6	2071	21	AA72184	DNA encoding human
14	253.6	62.6	2071	21	AA11622	Humanised HFE7A de
15	252	62.2	2073	21	AA11644	Humanised anti-Fas
16	252	62.2	2073	21	AA11645	Humanised anti-Fas
17	251.6	62.1	423	21	AA11646	Humanised anti-Fas
18	250.4	61.8	2073	21	AA11646	Humanised anti-Fas
19	248.8	61.4	457	19	AA70104	Humanised anti-Fas
20	248.8	61.4	457	21	AA72146	Humanised anti-Fas
21	248.8	61.4	457	21	AA11584	Humanised anti-Fas
22	248.8	61.4	2077	19	AA70079	Anti-Fas humanised
23	248.8	61.4	2077	21	AA72159	DNA encoding human
24	248.8	61.4	2077	21	AA11597	Humanised HFE7A de
25	248.2	61.3	405	21	AAAS9698	DNA encoding heavy
26	245.6	60.6	2077	21	AA11655	Humanised anti-Fas
27	245.2	60.5	423	21	AA11655	Humanised anti-Fas
28	245	60.5	405	20	AAV33947	Humanised antibody
29	245	60.5	405	22	AAV58738	Anti-CD33 antibody
30	245	60.5	411	21	AA44845	Murine M195 antibo
31	244.8	60.4	409	21	AA28738	CDNA encoding huma
32	244.8	60.4	409	22	AA70215	Anti-human VEGF re
33	243.4	60.1	405	19	AAV37264	CDNA encoding a va
34	243.4	60.1	405	21	AA295282	IgM chimeric antib
35	243.4	60.1	1773	18	AA288869	H chain subunit of
36	243.4	60.1	1773	19	AAV66735	Anti-human Fas mon
37	243.4	60.1	1773	21	AA78202	Anti-human Fas ant
38	242.2	59.8	478	20	AAV88433	EST clone GF196.
39	241.8	59.7	433	13	AAQ24790	Anti-Trc antibody
40	240.8	59.5	421	18	AA73624	CDNA for humanised
41	240.2	59.3	443	10	AAV91620	DNA sequence of th
42	240	59.3	409	21	AA287778	Anti-human VEGF re
43	240	59.3	409	22	AA70251	Anti-human Flt-1 a
44	239	59.0	418	19	AAV59116	HML.24 antibody he
45	239	59.0	418	19	AAV07581	Anti-human HML.24

## ALIGNMENTS

RESULT	1
AAAS9694	standard; DNA: 405 BP.
ID	AAAS9694;
AC	AAAS9694;
XX	14-NOV-2000 (first entry)
DT	
XX	
DE	DNA encoding heavy chain variable region of humanised 3S1 antibody.
XX	
XX	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW	autoimmune disease; infectious disease; inflammatory disorder;
KW	systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW	multiple sclerosis; transplant rejection; proliferative disease;
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome; ss.
XX	
OS	Synthetic.
OS	Mus sp.
OS	Homo sapiens.
XX	
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
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FT	/note= "no termination codon given"
FT	1..57
FT	/*tag= b
FT	mat_peptide
FT	58..405
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XX	

PN WO200047625-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 09-FEB-2000; 2000MO-US03303.  
 XX  
 PR 12-FEB-1999; 99US-0249011.  
 XX 24-JUN-1999; 99US-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GW;  
 XX  
 DR WPI: 2000-524532/47.  
 XX P-PSDB; AAB07965.  
 XX  
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 PS Example 3; Fig 2A; 162pp; English.  
 XX  
 CC The present sequence encodes the heavy chain variable region of the  
 CC humanized murine antibody 3D1. The antibody has a binding specificity to  
 CC B7 molecules. The antibody is used to construct humanized  
 CC immunoglobulins, which comprise an antigen binding region of non-human  
 CC origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulin, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX  
 SQ Sequence 405 BP; 102 A; 88 C; 110 G; 105 T; 0 other:  
  
 Query Match 100.0%; Score 405; DB 21; Length 405;  
 Best Local Similarity 100.0%; Pred. No. 1e-101;  
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
 ID AAA59692 standard; DNA; 405 BP.  
 XX  
 AC AAA59692;  
 XX  
 DT 14-NOV-2000 (first entry)  
 XX  
 DE Nucleotide sequence of heavy chain variable region of 3D1 antibody.  
 XX  
 KW Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;  
 KW autoimmune disease; infectious diseases; inflammatory disorder;  
 KW systemic lupus erythematosus; diabetes mellitus; insulin; asthma;  
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;  
 KW multiple sclerosis; transplant rejection; proliferative disease;  
 KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;  
 KW aplastic anaemia; myeloid dysplasia syndrome; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
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 FT /note= "no termination codon given"  
 FT sig-peptide 1..57  
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 PN WO200047625-A2.  
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 PD 17-AUG-2000.  
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 PF 09-FEB-2000; 2000MO-US03303.  
 XX  
 PR 12-FEB-1999; 99US-0249011.  
 XX 24-JUN-1999; 99US-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GW;  
 XX  
 DR WPI: 2000-524532/47.  
 XX P-PSDB; AAB07963.  
 XX  
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 PS Example 1; Fig 1A; 162pp; English.  
 XX  
 CC The present sequence encodes the heavy chain variable region of the  
 CC murine antibody 3D1. The antibody has a binding specificity to B7  
 CC molecules. The antibody is used to construct humanized immunoglobulins,  
 CC which comprise an antigen binding region of non-human origin and a  
 CC portion of a human immunoglobulin. The humanized immunoglobulins are  
 CC useful for treating autoimmune diseases, infectious diseases,  
 CC inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulin, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX  
 SQ Sequence 405 BP; 110 A; 89 C; 102 G; 104 T; 0 other:

Query Match 82.6%; Score 334.6; DB 21; Length 405;  
Best Local Similarity 89.1%; Pred. No. 2.2e-82;  
Matches 361; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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DB 1 atgggttggaactgatatcatcttcttcttggtttacacagctacaggtgtgactccag 60  
OY 61 gtccagctgtgctgctgtggtctgaggtgagaagcctgtggaagctcagtgaaagtgctc 120  
|||||  
DB 61 gtccagctgtgctgctgtggtcctgaggtgtgagcctgtggaagctcagtgaaagtgctc 120  
OY 121 tgcgaagcttcgctgctacacattcactgattatgctatcagtgagtgagagagctcct 180  
|||||  
DB 121 tgcgaaggtctcggctacacattcactgattatgctatcagtgagtgagagagctcct 180  
OY 181 ggaagggcctcggatgtgattgtgatttaatttacttgataataacacacacacacac 240  
|||||  
DB 181 gcaagagctcagagctgagatgtgagattatattacttacttgataataacacacacacac 240  
OY 241 cagaagtttaaggcacaagccacaatgactgtagacaagctgacagagacagcctatag 300  
|||||  
DB 241 cagaagtttaaggcacaagccacaatgactgtagacaagctgacagagacagcctatag 300  
OY 301 gaacttagtcttctgagatctgaggtacggtttattctctgtgcaagcggtcctg 360  
|||||  
DB 301 gaacttgccagatgacatctgaggtatctgcacattactctgtgcaagcggtcctg 360  
OY 361 tatatgactactggtggtcgaaggtacccctgtgacccgtctctca 405  
|||||  
DB 361 tatatgactactggtggtcgaaggtacccctgtgacccgtctctca 405

RESULT 3  
AAQ14802  
ID AAQ14802 standard; DNA: 524 BP.

AC AAQ14802;  
XX  
DT 13-FEB-1992 (first entry)  
XX  
DE Encodes murine anti-ICAM monoclonal antibody heavy chain.  
XX  
KW Interleukin adhesion molecule; variable region; V(H); mouse;  
KW R6-5-D6 murine MAb; complementarity determining region; CDR; ds.  
XX  
OS Mus musculus.

XX  
FH Key Location/Qualifiers  
FT sig\_peptide 34..90  
FT /\*tag= a  
FT /standard\_name= leader  
FT CDS 34..524  
FT /\*tag= b

PN W09116927-A.  
XX  
PD 14-NOV-1991.  
XX  
PE 29-APR-1991; 91WO-US02942.  
XX  
PR 27-APR-1990; 90GB-0009549.  
XX  
PA (CELL-) CELLTech LTD.  
PA (BOEH ) BOEHRINGER INGELHEIM PHA.  
XX  
PI Adair JR, Athwal DS, Rothlein RA;  
XX  
XX WPI; 1991-353533/48.  
XX  
XX P-PSDB; AARI5060.  
XX  
PT New humanised CDR-grafted anti-ICAM antibodies - used to treat

PT and prevent inflammation (e.g. psoriasis) tumours, viral  
PT infections and asthma and in diagnosis  
XX  
PS Disclosure: Fig 2; 83pp; English.

CC The heavy chain sequence was isolated from a cDNA library prepd. from  
CC hybridoma cell line R6-5-D6 which secretes murine IgG2a/Kappa  
CC antibody. The library was screened using a 980bp BamHI-EcoRI  
CC fragment of a previously isolated mouse IgG2a constant region  
CC clone. The murine framework-encoding sequences (i.e. not encoding  
CC CDRs) will be replaced by human framework sequences to produce  
CC recombinant (CDR-grafted humanised) antibody molecules having  
CC specificity for ICAM-1.  
XX  
SQ Sequence 524 BP; 128 A; 130 C; 131 T; 0 other;

Query Match 68.4%; Score 277.2; DB 12; Length 524;  
Best Local Similarity 81.4%; Pred. No. 1.4e-66;  
Matches 337; Conservative 0; Mismatches 66; Indels 9; Gaps 1;

OY 1 atgggttggaactgatatcatcttcttcttggtttacacagctacaggtgtgactccag 60  
|||||  
DB 34 atgggttggaactgatatcatcttcttcttggtttacacagctacaggtgtgactccag 93  
OY 61 gtccagctgtgctgctgtggtctgaggtgagaagcctgtggaagctcagtgaaagtgctc 120  
|||||  
DB 94 gtccagctgtgctgctgtggtcctgaggtgtgagcctgtggtctcagtgaaagtgctc 153  
OY 121 tgcgaagcttcgctgctacacattcactgattatgctatcagtgagtgagagagctcct 180  
|||||  
DB 154 tgcgaaggtctcggctacacattcactgattatgctatcagtgagtgagagagagctat 213  
OY 181 ggaagggcctcggatgtgattgtgatttaatttacttgataataacacacacacacac 240  
|||||  
DB 214 gcaagagctcagagctgagatgtgagattatattacttacttgcggtgacacacacacacac 273  
OY 241 cagaagtttaaggcacaagccacaatgactgtagacaagctgacagagacagcctatag 300  
|||||  
DB 274 cagaagtttaaggcacaagccacaatgactgtagacaagctgacagagacagcctatag 333  
OY 301 gaacttagtcttctgagatctgaggtacggtttattctctgtgcaagcggtcctg 360  
|||||  
DB 334 gaacttgccagatgacatctgaggtatctgcacattactctgtgcaagcggtcctg 393  
OY 361 -----tatatgactactggtggtcgaaggtacccctgtgacccgtctctca 405  
|||||  
DB 394 ttactactctcttctgactactggtggtcgaaggtacccctctcaagctctctca 447

RESULT 4  
AAQ14652  
ID AAQ14652 standard; cDNA: 524 BP.

AC AAQ14652;  
XX  
DT 14-FEB-1992 (first entry)  
XX  
DE R6-5-D6 anti-ICAM-1 heavy chain.  
XX  
KW Interleukin adhesion molecule-1; antibody; chimeric; ds.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT sig\_peptide 34..90  
FT /\*tag= a  
FT CDS 91..524  
FT /\*tag= b

PN W09116928-A.  
XX  
PD 14-NOV-1991.

XX	PF	29-APR-1991:	91WO-US02946.	
XX	PR	27-APR-1990:	90GB-0009548.	
XX	PA	(CELL-) CELLTECH LTD.		
XX	PA	(BOEH) BOEHRINGER INGELHEIM PHA.		
XX	PI	Adair JR, Robinson MK, Bright SM, Rothlein RA;		
XX	DR	WPI: 1991-353534/48.		
XX	DR	P-PSDB: AAR15200.		
PT	PT	New humanised chimeric anti-ICAM-1 antibodies - useful in		
PT	PT	treating inflammation e.g. psoriasis and ulcerative colitis to		
PT	PT	suppress metastasis of haematopoietic tumour cell and in		
PT	PT	diagnosis.		
XX	XX	Claim 10; Fig 2; 85pp; English.		
XX	XX			
CC	CC	The sequence comprises the 5' untranslated region, signal sequence,		
CC	CC	variable region and part of the constant region for the R6-5-6D		
CC	CC	murine MAb heavy chain. The hybridoma cell line R6-5-D6 producing		
CC	CC	the anti ICAM-1 Ab was provided by Boehringer Ingelheim		
CC	CC	Pharmaceuticals Inc. The cells were grown and mRNA isolated and		
CC	CC	used to prepare cDNA for a library in pSP64 vector DNA. The		
CC	CC	library was grown in E. coli LM1035 and colonies screened using a		
CC	CC	probe complementary to a sequence in the mouse kappa constant		
CC	CC	region or with a 980 bp BamHI-EcoRI restriction fragment of a		
CC	CC	previously isolated mouse IgG2a constant region clone. Ten		
CC	CC	positive clones were isolated and rescreened. Positive clones from		
CC	CC	the second round of screening were grown and the DNA inserts		
CC	CC	sequenced. The DNA was used to construct a humanised Abs having		
CC	CC	chimeric variable regions, esp. with IgG human constant region		
CC	CC	domains. The Abs can be used to treat inflammation, to suppress		
CC	CC	metastasis of haematopoietic tumour cells and growth of ICAM-1		
CC	CC	expressing tumour cells, to treat viral infection, to suppress		
CC	CC	extravascular migration of virally infected leucocytes and to treat		
CC	CC	asthma.		
CC	CC	See also AAQ14651 and AAQ14830.		
XX	XX			
SQ	SQ	Sequence 524 BP; 128 A; 130 C; 135 G; 131 T; 0 other;		
		Query Match 68.4%; Score 277.2; DB 12; Length 524;		
		Best Local Similarity 81.4%; Pred. No. 1.4e-66;		
		Matches 337; Conservative 0; Mismatches 68; Indels 9; Gaps		
				1.
QY	QY	1 atgggttgtaactgtatcatctctcttcttcgtgtaccacagctacaggtgtgacctccag 60		
DB	DB	34 atgggttcgtagctgtatcatctctcttcttcgtgtaccacagctacaggtgtgacctccag 93		
QY	QY	61 gtccgcctgtgtcagctctgtggctgtgagtggaagaagccctggagagctcagtggaagtgtcc 120		
DB	DB	94 gtccgcctgtgagcagctctgtggcctgtgaagctcgtggagcctgggtgtctcagtggaagtgtcc 153		
QY	QY	121 tgcnaagcttcgcgtgtacacatctgatatgtcatatacagltgggttgnaagaagcttct 180		
DB	DB	154 tgcnaaggttccggtacacatctgattgtatgtcatatacactgggttgnaagagagttcat 213		
QY	QY	181 ggcacgggcctcagatgtgattggaattatataattactatgatataataacaatacaac 240		
DB	DB	214 gcaaaagatctcagatgtgattggaattatataattactcctggtgacacaactataaac 273		
QY	QY	241 cagaagtttaagggaagccacaagtactgtagaacagtgacagacagacgtctatag 300		
DB	DB	274 cagaagtttaagggaagccacaagtactgtagaacagtgacagacagacgtctatag 333		
QY	QY	301t gaaactgtactctctgtagatctagaagatacagcgctttatctactgtgcaagacgagcttg 360		
DB	DB	334t gaaactgtcagattgacatcttgagatattctgtccatctatctactgtgcaagaggggagtg 393		
QY	QY	361 -----tatatgactactgggtgcaaggtacacctgttgacacggtctctca 405		

```

Db      394 ttactctccttgacctgagcggaaggccacacccttcacagtctctca   447
          |         |||         ||||    |||     |||||||||
RESULT  5 -----
AA005554 ID AA005554 standard; DNA: 446 BP.
AC        |         |
AA005554; |         |
DT        |         |
DE      10-DEC-1990 (first entry)
XX              |
XX Sequence encoding variable region of murine AHT 107 heavy chain.
XX Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
OS Mus sp.
XX           |
XX Key       | Location/Qualifiers
FH CDS       | 45..446
FT CD5       | /*tag= a
                |
EP380068-A.   |
PN            |
PD      01-AUG-1990.
XX             |
PF      24-JAN-1990; 90EP-0101351.
XX             |
PR      04-DEC-1989; 89US-0441702.
PR      24-JAN-1989; 89US-0301216.
XX             |
PA (MOLE-) MOLECULAR THERAPEU.
XX             |
XX Zerler B;
PI           |
DR WPI: 1990-232892/31.
P-PSDB; AAR06250;
PT Expression vectors for producing chimeric monoclonal antibodies -
PP which express human constant region and non-human variable region
PS Disclosure; ; P; English.
XX
CC MAb's comprising mouse CH and CL constant regions which human
CC variable regions may be used to create mouse/human hybrid MAbs,
CC which have a longer serum half-life. Method can be used to produce
CC Abs against interleukin-2 receptor and tumour necrosis factor.
XX
SQ Sequence 446 BP; 117 A; 110 G; 113 G; 106 T; 0 other;

Query Match      67.2%; Score 272.2; DB 11; Length 446;
Best Local Similarity 81.2%; Pred. No. 3,1e+65;
Matches 329; Conservative 0; Mismatches 73; Indels 3; Gaps
QY      1 atgggttggaaatgcatacatctttcttgtgttacacagctaagaigtgtaactccaag 60
Dy      45 atgggctggaggtgatcatactctcttgtgcgaacaagctaacagattgcactcccag 104
QY      61 gtccagctgggtgcattctcggggtctgagtgaaaagcctggggagctcagtgaaagtgtcc 120
Dy      105 gtcscagctgcacagatctcgggctcgtgaagtgvtgaagcctgggtgtccagtyaaagatticc 164
QY      121 tgcgaagcttcgccggtcacatatctactgattatggtacagtggtgtagacagcttcct 180
Dy      165 tgcaaaggtttccgcgtacacattcacatctatattatgcttcgcgaactgggtgaagcagaatcat 224
QY      181 ggacacagggccttcgaattggaattggaattttaaatattactatgataataacatacaactacaac 240
Dy      225 gccaaagagtctcagattggttatgtaattatgtcttcttaaactaygtgtacaagaactaac 284
QY      241 cagaagtttaaggcgaaggccacaatgatgctgtagacaaagtcgaagcagaagcctatatg 300

```



CC activity and can be used to treat autoimmune diseases, especially  
 CC rheumatism. The IgM molecule used in the invention are human Fas-antigen  
 CC binding properties. Included in the invention are nucleotide sequences  
 CC of the IgM light and heavy chains (see AAW78267-A78272) and the  
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
 CC AAW8202-A78206) and protein sequences (see AAB12908-B12910). Also  
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
 CC Primers specific for the invention are represented by sequences  
 CC chains used in the invention are represented by sequences  
 CC AAW8213-A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AAW8277-A78318 and  
 CC AAW8335-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
 CC represented by sequences AAW8321-A78334 and AAW8338-A78367. Primer  
 CC sequences AAW8207-A78212 are specific for murine Ig DNA, and are used in  
 CC the production of the agent of the invention.

XX Sequence 1767 BP; 384 A; 568 C; 485 G; 330 T; 0 other;

#### Query Match

Best Local Similarity 65.6%; Score 265.8; DB 21; Length 1767;  
 Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatcttcttctgtgtaccacagctacaggtgtcacctccag 60  
 DB 1 atgggattgagctgtactcttctctctccctccaggaactcagcgctccacttgag 60  
 QY 61 gtccacactgtgtgagctgtggtggtggaagaacccgtggagcccaagtgaggtcc 120  
 DB 61 gtgcagctctgtgagctgtggtggtggaagaacccgtggagcccaagtgaggtcc 120  
 QY 121 tggaaagctccgagccacatcattatgatacagtgaggtggaagagctcc 180  
 DB 121 tggaaagctctgtgatacactcactgactataatgaggtgtggtccgagccccc 180  
 QY 181 ggaacagggcctcagtgagtgagtgatgaatgaatgaatgaatgaatgaatgaat 240  
 DB 181 ggaacagggcctcagtgagtgagtgatgaatgaatgaatgaatgaatgaatgaat 240  
 QY 241 cagaagtttaaggcagaagcccaatgactgtgatacagtcgagccgaagctatag 300  
 DB 241 cagaagttcaagcagaagcccaatgactgtgatacagtcgagccgaagctatag 300  
 QY 301 gaactagttcttggagctgaggaagcagcgtttattactgtcgaagaagcgctcg 360  
 DB 301 gaactagttcttggagctgaggaagcagcgtttattactgtcgaagaagcgctcg 360  
 QY 361 tataaggaactcgtgggtcgaaggtacccctgttcacgcgtccctca 405  
 DB 361 gcataggaactcgtgggtcgaaggtacccctgttcacgcgtccctca 405

#### RESULT 8

AAV61364  
 ID AAV61364 standard; cDNA to mRNA; 1768 BP.

AC AAV61364;

DT 18-JAN-1999 (first entry)

DE Anti-human Fas humanised antibody CH11 heavy chain Humu cDNA.

XX Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;

KW autoimmune disease; rheumatoid arthritis; therapy; human;

KW antibody engineering; ds.

OS Homo sapiens.

XX Synthetic.

FT Key Location/Qualifiers  
 CDS 1..1767  
 FT /\*tag= a

FT sig\_peptide 1..57  
 FT /\*tag= b  
 FT mat\_peptide 58..1764  
 FT /\*tag= c

XX EP866131-A2.

XX 23-SEP-1998.

PF 20-MAR-1998; 98EP-0302113.

PR 21-MAR-1997; 97JP-0067938.

PA (SANY ) SANKYO CO LTD.

PI Haruyama H, Nakahara K, Serizawa N, Takahashi T;

PI Yonehara S;

DR WPI; 1998-482965/42.

DR P-PSDB; AAW71881

PT Production of anti-Fas protein humanised antibodies - for use in  
 PT inducing apoptosis on Fas expressing cells in the treatment of  
 PT autoimmune diseases, especially rheumatoid arthritis

XX Example 3: Page 108-110; 187pp; English.

CC This cDNA sequence codes for a humanised anti-Fas antibody CH11  
 CC heavy chain (see AAW71881), designated Humu. Humu is based on the  
 CC light chain (see AAW71888) of murine anti-human Fas monoclonal  
 CC antibody CH11. The humanised sequence was designed following  
 CC selection of donor residues from CH11 to be grafted onto acceptor  
 CC molecule 21.28/CL. 2 light chain sequences (see AAW71880-81) have  
 CC been designed, and each can be used in combination with any of 4  
 CC light chain sequences (see AAW71876-79) to provide novel, claimed  
 CC humanised CH11 IgM antibodies that lack a J chain. These humanised  
 CC anti-human Fas antibodies are capable of inducing apoptosis in cells  
 CC expressing Fas (e.g. synovialocytes) and are useful in the treatment  
 CC of autoimmune disease and chronic rheumatoid arthritis. DNA  
 CC vectors encoding the humanised antibodies are claimed, as are  
 CC sequences such as pHumu1-1 including the Humu nucleotide sequence,  
 CC and host cells such as Escherichia coli pHumu1-1 (FERM BP-5864).

XX Sequence 1768 BP; 387 A; 564 C; 485 G; 332 T; 0 other;

#### Query Match

Best Local Similarity 65.6%; Score 265.8; DB 19; Length 1768;  
 Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatcttcttctgtgtaccacagctacaggtgtcacctccag 60  
 DB 1 atgggattgagctgtactcttctctctccctccaggaactcagcgctccacttgag 60  
 QY 61 gtccacactgtgtgagctgtggtggtggaagaacccgtggagcccaagtgaggtcc 120  
 DB 61 gtgcagctctgtgagctgtggtggtggaagaacccgtggagcccaagtgaggtcc 120  
 QY 121 tggaaagctccgagccacatcattatgatacagtgaggtggaagagctcc 180  
 DB 121 tggaaagctctgtgatacactcactgactataatgaggtgtggtcgaagaagcgct 180  
 QY 181 ggaacagggcctcagtgagtgagtgatgaatgaatgaatgaatgaatgaatgaat 240  
 DB 181 ggaacagggcctcagtgagtgagtgatgaatgaatgaatgaatgaatgaatgaat 240  
 QY 241 cagaagtttaaggcagaagcccaatgactgtgatacagtcgagccgaagctatag 300  
 DB 241 cagaagttcaagcagaagcccaatgactgtgatacagtcgagccgaagctatag 300  
 QY 301 gaactagttcttggagctgaggaagcagcgtttattactgtcgaagaagcgctcg 360  
 DB 301 gaactagttcttggagctgaggaagcagcgtttattactgtcgaagaagcgctcg 360



QY 361 tatatgactactggtggtcagggtacccctgtccctccca 405  
|||||  
Db 361 gctatgactactggtggtcagggtacccctgtccctccca 405

RESULT 9  
AAA78272  
ID AAA78272 standard; DNA: 1768 BP.  
XX  
AC AAA78272:  
XX  
DT 16-NOV-2000 (first entry)  
XX  
DE Anti-human Fas immunoglobulin M heavy chain DNA sequence SEQ ID #87.  
XX  
KW Antihumetic agent; immunoglobulin M; IgM; apoptosis inducer;  
KM immunosuppression; autoimmune disease; treatment; rheumatism;  
KW anti-Fas antibody; ss.  
XX  
OS Synthetic.  
XX  
PN JP2000154149-A.  
XX  
PD 06-JUN-2000.  
XX  
PF 17-SEP-1999; 99JP-0263984.  
XX  
PR 18-SEP-1998; 98JP-0264598.  
XX  
PA (SANY ) SANKYO CO LTD.  
XX  
DR WPI: 2000-454476/40.  
XX  
DR P-PSDB; AAB12918.  
XX  
PT Anti-human Fas humanizing antibody-containing antirheumatic agents  
XX  
PS Example 2; Page 77-79; 109pp; Japanese.  
XX  
CC The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
CC binding properties. Included in the invention are nucleotide sequences  
CC of the IgM light and heavy chains (see AAB78267-A78272) and the  
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
CC nucleotide sequences of the humanised anti-human Fas Ig CH1 (see  
CC AAB78202-A78206) and protein sequences (see AAB12908-B12910). Also  
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
CC chains used in the invention are represented by sequences  
CC AAB78213-A78266. Primers used for sequencing the human Ig DNA used in the  
CC invention are represented by sequences AAB78277-A78318 and  
CC AAB78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
CC represented by sequences AAB78321-A78334 and AAB78338-A78367. Primer  
CC sequences AAB78207-A78212 are specific for murine Ig DNA, and are used in  
CC the production of the agent of the invention.  
XX  
SQ Sequence 1768 BP; 387 A; 564 C; 485 G; 332 T; 0 other;

Query Match 65.6%; Score 265.8; DB 21; Length 1768;  
Best Local Similarity 78.5%; Pred. No. 2.5e-63;  
Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctctcttctgtgtaccacaggtacaggtgacatccacg 60  
|||||  
Db 1 atgggttggaactgtatctctctctctctctctcgtcaggaactgtcaggtgacatccg 60  
61 gtccagctgtgtcagctgtggtggtgaggtgaagaagctgtggaagctcagtggaagtgtcc 120

Db 61 gtgcagctgtgcagctctggtggtcagggtgaagaagctgtggtcagtggaaggttcc 120  
QY 121 tgcagaagctccggctacacattacatgattatgctacagtggtggaagcagctccct 180  
|||||  
Db 121 tgcagaagctccggctacacattacatgattatgctacagtggtggaagcagctccct 180  
QY 181 ggcagaagctccggctacagtgattatgattataattactactgataataacaaataaac 240  
|||||  
Db 181 ggcagaagctccggctacagtgattatgattataattactactgataataacaaataaac 240  
QY 241 cagaagcttcaaggcagaagccacacattactgttagacaaagtcgaagcagcctataatg 300  
|||||  
Db 241 cagaagcttcaaggcagaagccacacattactgttagacaaatccgcgacagcctataatg 300  
QY 301 gaacttagctctcttgagatcctggaagatcgaagcagcgttattactgtgcaagagcgttgg 360  
|||||  
Db 301 gactgtgagcagcctgtgagatcctggaagcagcgttattactgtgcaagagcgttactat 360  
QY 361 tatatgactactggtggtcagggtacccctgtccctccca 405  
|||||  
Db 361 gctatgactactggtggtcagggtacccctgtccctccca 405

RESULT 10  
AAT42717  
ID AAT42717 standard; DNA: 424 BP.  
XX  
AC AAT42717:  
XX  
DT 04-FEB-1997 (first entry)  
XX  
DE HUMC3 VH coding sequence.  
XX  
KW Humanised antibody; variable heavy region; buried residue modification;  
KW VH: HUMC3 VH: BA46 antigen; human; milk fat globule; HMG; lactation;  
KW fat globule membrane; murine; mammary epithelial cell; breast cancer;  
KW breast membrane glycoprotein; therapy; immunotherapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 11..418  
FT /\*tag= a  
FT /product= HUMC3 VH (BR-M version)  
XX  
PN MO9608565-A2.  
XX  
PD 21-MAR-1996.  
XX  
PF 14-SEP-1995; 95WO-US11683.  
XX  
PR 07-JUN-1995; 95US-0487598.  
PR 16-SEP-1994; 94US-0307668.  
XX  
PA (CANC-) CANCER RES FUND CONTRA COSTA.  
XX  
PI Certani RI, Do Couto FJR, Peterson JA;  
XX  
DR WPI: 1996-179941/18.  
XX  
DR P-PSDB; AAW06442.  
XX  
PT Recombinant Mc3 antibody which binds BA46 antigen of HMG -  
XX  
PS the diagnosis and therapy of breast cancer  
XX  
PS Claim 13; Fig 18; 91pp; English.  
XX  
CC This sequence represents the coding sequence for the variable heavy (VH)  
CC chain of the humanised murine antibody HUMC3 VH. The Mc3 VH sequence was  
CC humanised using the buried residue modification technique, where  
CC important non-human framework residues are unaffected. The Mc3 antibody  
CC binds to the BA46 antigen of the human milk fat globule (HMG). The milk

CC fat globule membrane is derived from the apical surface of the mammalian  
CC epithelial cell during lactation, and therefore is a source for breast  
CC membrane glycoproteins. The antibody can be used in an in vitro method  
CC to detect a HmFG antigen (or antigen fragment), and to diagnose the  
CC presence of the antigen in a subject. The antibody can also be used to  
CC deliver an agent to a target (within a subjects body), containing a HmFG  
CC antigen. The antibodies can also be used for diagnosis, prognosis, and  
CC therapeutic applications of breast cancer. As the humanised antibodies  
CC retain their high affinity binding to the antigen, they are useful for  
CC immunodiagnostic and immunotherapeutic applications in humans.  
XX  
SQ Sequence 424 BP; 106 A; 102 C; 112 G; 104 T; 0 other;

Query Match 62.8%; Score 254.4; DB 17; Length 424;  
Best Local Similarity 78.2%; Pred. No. 2.3e-60;  
Matches 319; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

QY 1 atgggttggaactgtatcatctcttctgtgtacacagctacaggtgtgactccag 60  
DB 11 atgaaatgacagctgtgcatctctctctctcgtcaggaactgtcagctcctgag 70  
QY 61 gtccagctgtgtcagctgtgtggtcgaagtgaagaagcctggagctcagtgatc 120  
DB 71 gtccagctgtgtcagctgtgtggtcgaagtgaagaagcctggagctcagtgatc 130  
QY 121 tgcgaagcttcgcgcctacacatctacatgattatgatacagttggtagcagctct 180  
DB 131 tgcgaagcttcgtttatcatctacacagctacacagcctggtagaagcagccct 190  
QY 181 ggaacaggcctcgcagctgtgattggaattataatattatgataataacaactaac 240  
DB 191 ggaatgaacctgtgattgattggaattataatattatgataatacaatgtgtac 250  
QY 241 cagaagtttaaggcgaagccacaatgactgtagaacaagtgcagagacagctctat 300  
DB 251 cagaagttccaggaacagccacaatgactgtagaacaagtgcagagacagctctat 310  
QY 301 gaacttagcttcgtgagatcgtagatagcgccttatactgtgcaagagcgccctg 360  
DB 311 gagctcagcagctcgtgagatcgtgagatagcgccttatactgtgcaagagcgct 370  
QY 361 ta---tatgactactcgtgggtcaaggtacccctgtcacgcgtctctca 405  
DB 371 tatactatgactatctgggtcaaggaacctgtgcaccgtctctca 418

## RESULT 11

AA066702 standard; cDNA; 451 BP.

AA066702 standard; cDNA; 451 BP.

16-NOV-1994 (first entry)

DREG-200 Humanized antibody heavy chain variable region.

DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1;

humanized antibody; immunoglobulin; Ig; IgG1; IgG4;

framework; light chain; heavy chain; variable domain;

monoclonal antibody; acceptor antibody Eu; transgenic animal; ss.

Mus sp.; Homo sapiens.

Key Location/Qualifiers

CDS 12..434

sig\_peptide 12..68

mat\_peptide 69..431

/\*tag- a

/\*tag- b

/\*tag- c

PN W09412215-A.  
XX 09-JUN-1994.  
PD 30-NOV-1993; 93WO-0511612.  
XX 01-DEC-1992; 92US-0983946.  
XX (PROT-) PROTEIN DESIGN LABS INC.  
PA Co MS;  
PI WPI; 1994-19974/24.  
DR P-PSDB; AAR55556.  
XX New humanised antibody specific for L-selectin - with murine CDR  
PT and human framework regions, inhibits binding of neutrophils to  
PT endothelial cells and useful for treating or preventing  
PT inflammation  
PS Disclosure; Fig. 3B; 60pp; English.

CC An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs  
CC corresponding to those of mouse Mab DREG-200 and heavy and light  
CC chain variable region frameworks of the human acceptor antibody Eu.  
CC Nucleotide and aa sequences are provided for the DREG-200 light  
CC (AA066699, AAR55553) and heavy (AA066700, AAR55554) chain variable  
CC regions and the humanized DREG-200 light (AA066701, AAR55555) and heavy  
CC (AA066702, AAR55556) chain variable regions. The humanized antibodies  
CC can be produced economically in large quantities by expression in  
CC mammalian cell culture or in transgenic animals.  
XX  
SQ Sequence 451 BP; 120 A; 105 C; 116 G; 110 T; 0 other;

Query Match 62.6%; Score 253.6; DB 15; Length 451;  
Best Local Similarity 77.6%; Pred. No. 4e-60;  
Matches 326; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

QY 1 atgggttggaactgtatcatctcttctgtgtacacagctacaggtgtgactccag 60  
DB 12 atgggttggaactgtatcatctctctctctgtgtacacagctacaggtgtgactccag 71  
QY 61 gtccagctgtgtcagctgtgtggtcgaagtgaagaagcctggagctcagtgatc 120  
DB 72 gtccagctgtgtcagctgtgtggtcgaagtgaagaagcctggagctcagtgatc 131  
QY 121 tgcgaagcttcgcgcctacacatctacatgattatgatacagttggtagcagctct 180  
DB 132 tgcgaagcttcgtatcacatctacatgattatgatacagttggtagcagctct 191  
QY 181 ggaacaggcctcgcagctgtgattggaattataatattatgataataacaactaac 240  
DB 192 ggtcaagagctcgtgattgattatattatcttcaatagttgttacaagaataac 251  
QY 241 cagaagtttaaggcgaagccacaatgactgtagaacaagtgcagagacagctctat 300  
DB 252 gagaagtttcaaggcgcagcagcacaatctcagcagcagcacaatcagcagctat 311  
QY 301 gaacttagcttcgtgagatcgtagatagcgccttatactgtgcaagagcgccct- 358  
DB 312 gaactcagcagctcgtgagatcgtgagatcgtgcaatctatctatctgtgcaagagagat 371  
QY 359 -----ggtatagactactcgtgggtcaaggtacccctgtcacgcgtctctca 405  
DB 372 ggtactacagctcgtgactcgtatctgtgtggtcgaaggtacacgtgcacagctctca 431

## RESULT 12

AAV70080 standard; DNA; 2071 BP.

AAV70080;



KW murine: humanised antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; heavy chain; ds.  
 XX Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX Jp2000169393-A.  
 XX 20-JUN-2000.  
 PD 30-SEP-1999; 99JP-0278301.  
 PF 30-SEP-1998; 98JP-0276883.  
 PR (SANKYO) SANKYO CO LTD.  
 PA WPI: 2000-485645/43.  
 DR P-PSDB: AAB14779.  
 XX Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 XX Example 22; Page 106-108; 139pp; Japanese.  
 PS The invention relates to compositions for the prevention or treatment  
 CC of diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The compositions of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences AAA72146, AAA72159 and AAA72184  
 CC represent DNA encoding the heavy chains (or fragments thereof) of  
 CC various humanised HFE7A-derived anti-Fas antibodies.  
 XX  
 SQ Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;  
 Query Match 62.6%; Score 253.6; DB 21; Length 2071;  
 Best Local Similarity 77.6%; Pred. No. 5,9e-60;  
 Matches 326; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

QY 352 -----gcggcctgtatagactcgtgggtcaaggtaacctgtcacccgtccca 405  
 Db 361 tatagtaacaactgactcgtcgtcgggcgaaggaccctggtcacccgtccca 440  
 RESULT 14  
 ID AAA11622 standard; DNA: 2071 BP.  
 AC AAA11622;  
 XX 08-AUG-2000 (first entry)  
 DE Humanised HFE7A designed heavy chain DNA #2.  
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.  
 XX Synthetic.  
 OS EP990663-A2.  
 XX 05-APR-2000.  
 PD 29-SEP-1999; 99EP-0307711.  
 PF 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX (SANKYO) SANKYO CO LTD.  
 PA Serizawa N, Hattuyama H, Nakahara K, Tamaki I, Takahashi T;  
 PI WPI: 2000-258930/23.  
 DR P-PSDB: AAW90929.  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX Example reference 22; Page 148-150; 263pp; English.  
 PS This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (II) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal

cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence encodes a humanised anti-Fas antibody HFE7A designed heavy chain which is used in the method described in the invention.

Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;

Query Match 62.6%; Score 253.6; DB 21; Length 2071;  
Best Local Similarity 77.6%; Pred. No. 5,9e-60;  
Matches 326; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

```
OY 1 atgggttggaactatcatcttcttctgtaccacagctgagtgactccag 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 atggagtggagctgtatcatctctctgtgtagcaacagctgagtcacag 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 gtccagctggtgacgtctggggtcgtgaagaagcctggagctcagtgagttcc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 gtccaactggtgacgtctggggtcgtgaagaagcctgggcttcagtgaaagttcc 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 tgcgaagcttcggtacacatcgtatctatctacagctggtgagcagctcct 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 141 tgcgaagcttcgtgtacacatcgtatctacagctggtgagcagctcct 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 ggacagggcctcgtggtggtggtatataatcttactgtatacaatacacaac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 201 ggacagggcctcgtggtggtggtggtatataatcttactgtatacaatacacaac 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 cagaagtttaaggcgaagggcacacatgactgtagaacaagtcgaagcagcagctatgt 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 261 caaagttcaaggcgaagggcacacatgactgtagaacaagtcgaagcagcagctatgt 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 301 gaaactagcttctgagatcgtgagatagcgccgtttactgtgcaaga----- 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 321 gagctcagcagcgtgagatcgtgagacggcggtctctactgtgcaagaataaggac 380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 352 -----gcggcctgtatagactactgggtggaaggtaccctgttaccggtctcca 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 381 tatagtaaacactgttactcgtactggtcgtggcggaaggacccctggtacacgtctcccca 440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

## RESULT 15

AAAI1644 standard; DNA; 2073 BP.

AAAI1644;

08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Neu 1 DNA.

Fas: antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
dermatological; immunosuppressive; chylomicretic; antirheumatic; anti-Fas;  
neurotrophic; antinfertility; neuroprotective; antiarteriosclerotic;  
hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
Storjen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.

Synthetic.

EP990663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

PA (SANY ) SANKYO CO LTD.

PI Serizawa N, Haryama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI: 2000-258930/23.

DR P-PSDB: AAW90933.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
inflammatory or autoimmune disease, induces apoptosis selectively in  
cells with abnormal Fas-Fas ligand systems

Claim 33; Page 166-168; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thymomimetic, antirheumatic, nephrotropic, antinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Storjen's syndrome, peritonsils or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence encodes a humanised anti-Fas antibody heavy chain construct designated Neu 1 which is described in the method of the invention.

Sequence 2073 BP; 462 A; 685 C; 559 G; 367 T; 0 other;

Query Match 62.2%; Score 252; DB 21; Length 2073;  
Best Local Similarity 77.4%; Pred. No. 1.6e-59;  
Matches 325; Conservative 0; Mismatches 80; Indels 15; Gaps 1;

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OY 1 atgggttggaactatcatcttcttctgtaccacagctgagtgactccag 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 23 atggagtggagctgtatcatctctctgtgtagcaacagctgagtcacag 82
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 gtccagctggtgacgtctggggtcgtgaagaagcctggagctcagtgagttcc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 83 gtccaactggtgacgtctggggtcgtgaagaagcctgggcttcagtgaaagttcc 142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 tgcgaagcttcggtacacatcgtatctatctacagctggtgagcagctcct 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 143 tgcgaagcttcgtgtacacatcgtatctatctacagctggtgagcagctcct 202
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 ggacagggcctcgtggtggtggtggtatataatcttactgtatacaatacacaac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 203 ggacagggcctcgtggtggtggtggtggtatataatcttactgtatacaatacacaac 262
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 cagaagtttaaggcgaagggcacacatgactgtagaacaagtcgaagcagcagctatgt 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 263 caaagttcaaggcgaagggcacacatgactgtagaacaagtcgaagcagcagctatgt 322
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 301 gaaactagcttctgagatcgtgagatagcgccgtttactgtgcaaga----- 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 323 gagctcagcagcctgagatctgaggacacggcggtctattactgtgcaagaataagggac 382  
Oy 352 -----gcggcctgtgtatggaacttgagggtcaaggttaacctgtgcacccgtctcctca 405  
Db 383 tatagtacaactcgtgtactcgcgtgtgtggtggtccaaaggtacactgtgcacccgtctcctca 442

Search completed: August 26, 2002, 16:19:48  
Job time: 4482 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 15:04:11 ; Search time 60.31 Seconds

(without alignments)  
1649.504 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405  
Sequence: 1 atgggttgagactgcatcatc.....cccttgccaccctcctca 405

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 363533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/prodata/2/lna/5A.COMB.seq: \*  
2: /cgn2\_6/prodata/2/lna/5B.COMB.seq: \*  
3: /cgn2\_6/prodata/2/lna/5A.COMB.seq: \*  
4: /cgn2\_6/prodata/2/lna/5B.COMB.seq: \*  
5: /cgn2\_6/prodata/2/lna/PCUS.COMB.seq: \*  
6: /cgn2\_6/prodata/2/lna/Backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277.2	68.4	524	5	Sequence 4, Appl 1
2	254.4	62.8	424	4	Sequence 62, Appl 1
3	253.6	62.6	451	4	Sequence 11, Appl 1
4	253.6	62.6	451	5	Sequence 11, Appl 1
5	248.2	61.3	433	1	Sequence 11, Appl 1
6	248.2	61.3	433	1	Sequence 11, Appl 1
7	245	60.5	405	1	Sequence 68, Appl 1
8	245	60.5	405	1	Sequence 68, Appl 1
9	245	60.5	405	1	Sequence 68, Appl 1
10	245	60.5	405	1	Sequence 68, Appl 1
11	245	60.5	405	1	Sequence 68, Appl 1
12	240.8	59.5	421	3	Sequence 62, Appl 1
13	238.6	58.9	433	1	Sequence 18, Appl 1
14	238.6	58.9	433	1	Sequence 18, Appl 1
15	238.6	58.9	433	1	Sequence 18, Appl 1
16	238.6	58.9	433	1	Sequence 18, Appl 1
17	238.6	58.9	433	4	Sequence 18, Appl 1
18	237.6	58.7	422	1	Sequence 77, Appl 1
19	237.6	58.7	422	1	Sequence 77, Appl 1
20	237.6	58.7	422	2	Sequence 77, Appl 1
21	237.6	58.7	422	2	Sequence 77, Appl 1
22	237.6	58.7	422	2	Sequence 77, Appl 1
23	237.6	58.7	422	2	Sequence 77, Appl 1
24	237.6	58.7	422	2	Sequence 77, Appl 1
25	237.6	58.7	422	2	Sequence 77, Appl 1
26	236.8	58.5	409	4	Sequence 98, Appl 1
27	236	58.3	421	3	Sequence 73, Appl 1

28	234.4	57.9	421	3	US-08-836-561-77	Sequence 77, Appl 1
29	233.6	57.7	408	5	PCT-US91-11611-3	Sequence 3, Appl 1
30	232.8	57.5	429	1	US-08-236-520-6	Sequence 6, Appl 1
31	232.8	57.5	429	5	PCT-US91-05262-6	Sequence 26, Appl 1
32	232.2	57.3	405	1	US-08-137-117D-26	Sequence 26, Appl 1
33	232.2	57.3	405	1	US-08-436-717-26	Sequence 26, Appl 1
34	231.4	57.1	461	2	US-07-916-098A-39	Sequence 39, Appl 1
35	231.4	57.1	2560	2	US-07-916-098A-44	Sequence 44, Appl 1
36	229.6	56.7	433	3	US-08-673-799C-99	Sequence 82, Appl 1
37	229.6	56.7	421	3	US-08-836-561-82	Sequence 60, Appl 1
38	229.4	56.6	432	2	US-08-483-528B-60	Sequence 60, Appl 1
39	229.4	56.6	432	2	US-08-673-799C-60	Sequence 3, Appl 1
40	227.4	56.1	461	4	US-09-096-244-3	Sequence 11, Appl 1
41	227	56.0	386	4	US-09-199-149-11	Sequence 23, Appl 1
42	227	56.0	1572	1	US-08-353-400-23	Sequence 100, Appl 1
43	226.2	55.9	433	3	US-08-673-799C-100	Sequence 101, Appl 1
44	226.2	55.9	433	3	US-08-673-799C-101	Sequence 84, Appl 1
45	226	55.8	414	1	US-07-634-278-84	

## ALIGNMENTS

RESULT 1  
PCT-US91-02942-4  
; Sequence 4, Application PC/TUS9102942  
; GENERAL INFORMATION:  
; APPLICANT: ROTHLEIN, ROBERT  
; APPLICANT: ADAIR, JOHN R  
; APPLICANT: ATHAL, DILJEET S  
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Ave. NW Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/02942  
; FILING DATE: 19910429  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9009549.8  
; FILING DATE: 27-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOX, SAM L  
; REGISTRATION NUMBER: 30,353  
; REFERENCE/DOCKET NUMBER: 1011.0586600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 466-0800  
; TELEFAX: (202) 833-8716  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 524 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: Both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 34..522  
; PCT-US91-02942-4

Query Match 68.4%; Score 277.2; DB 5; Length 524;  
Best Local Similarity 81.4%; Pred. No. 3.2e-81;





ATTORNEY/AGENT INFORMATION:  
NAME: Liebescheut, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 12..431  
US-08-579-378A-11

Query Match 62.6%; Score 253.6; DB 4; Length 451;  
Best Local Similarity 77.6%; Pred. No. 1.5e-73;  
Matches 326; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgttaccacagctaacagtgctccag 60  
DB 12 ATGGGATGGAGCTGTATCATCTCTCTGTGTAGCAACAGCTACAGGTCTCCAG 71  
QY 61 gtccagctgtgacgtctggagctgaagtgaaagcctggagctcagtgaaagtcc 120  
DB 72 GTCCAGCTGTGACAGTGTGAGCTGAAGTCAAGAACTGGAGCTCAGTGAAGTATCC 131  
QY 121 tgcgaagcttcgagctacacattcattatgctatacagtggtgagacagctcct 180  
DB 132 TGCAGAGCTTCTGTGATACATTCACATTCAGTATGTATGCACTGGTGAGACAGCACT 191  
QY 181 ggaagagcctcgaagtgtgagttgagtttaatttactatgataatacaactaac 240  
DB 192 GGTCAAGAGACTCGATGGATTGGATATTTATCTTACAAATGATGTTACCAAGTACAT 251  
QY 241 cagaagtttaagggcaagccacaatgactgtagacaagtgacagacacagctatag 300  
DB 252 GAGAAGTTCAAAAGCCGAGTCACAAATTAATTACAGACGAGTCAACACAGCCTACATG 311  
QY 301 gaactagttcttgagatctgagatacagcgcttatactgctcaagagcgacct- 358  
DB 312 GAACCTGACAGCTTGCGATCGGAGACACGCACTTATTACTGTGCAAGGAGGAGTAT 371  
QY 359 -----gatatagactactggggtcaaggttaacctgtgcaagcgtctctca 405  
DB 372 GGTACTACGTTGCGTACTTCGATGTCTGGGGCCCAAGGTACACTGTGTCACAGTCTCTCA 431

RESULT 4  
PCT-US93-11612-11  
Sequence 11, Application PC/TUS9311612  
GENERAL INFORMATION:  
APPLICANT: Co. Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11612  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 451 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 12..431  
PCT-US93-11612-11

Query Match 62.6%; Score 253.6; DB 5; Length 451;  
Best Local Similarity 77.6%; Pred. No. 1.5e-73;  
Matches 326; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgttaccacagctaacagtgctccag 60  
DB 12 ATGGGATGGAGCTGTATCATCTCTCTGTGTAGCAACAGCTACAGGTCTCCAG 71  
QY 61 gtccagctgtgacgtctggagctgaagtgaaagcctggagctcagtgaaagtcc 120  
DB 72 GTCCAGCTGTGACAGTGTGAGCTGAAGTCAAGAACTGGAGCTCAGTGAAGTATCC 131  
QY 121 tgcgaagcttcgagctacacattcattatgctatacagtggtgagacagctcct 180  
DB 132 TGCAGAGCTTCTGTGATACATTCACATTCAGTATGTATGCACTGGTGAGACAGCACT 191  
QY 181 ggaagagcctcgaagtgtgagttgagtttaatttactatgataatacaactaac 240  
DB 192 GGTCAAGAGACTCGATGGATTGGATATTTATCTTACAAATGATGTTACCAAGTACAT 251  
QY 241 cagaagtttaagggcaagccacaatgactgtagacaagtcgaagacacagctatag 300  
DB 252 GAGAAGTTCAAAAGCCGAGTCACAAATTAATTACAGACGAGTCAACACAGCCTACATG 311  
QY 301 gaactagttcttgagatctgagatacagcgcttatactgctcaagagcgacct- 358  
DB 312 GAACCTGACAGCTTGCGATCGGAGACACGCACTTATTACTGTGCAAGGAGGAGTAT 371  
QY 359 -----gatatagactactggggtcaaggttaacctgtgcaagcgtctctca 405  
DB 372 GGTACTACGTTGCGTACTTCGATGTCTGGGGCCCAAGGTACACTGTGTCACAGTCTCTCA 431

RESULT 5  
US-08-137-117D-111  
Sequence 11, Application US/08137117D  
Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 158

```

CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 16..420
NAME/KEY: mat_peptide
LOCATION: 16..420
US-08-137-117D-111

Query Match      61.3%; Score 248.2; DB 1; Length 433;
Best Local Similarity 75.8%; Pred. No. 8,7e-72;
Matches 307; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 atgggttggaactgtatcatctctctctgtttacacagctacaggtgtgactccag 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 16 ATGACACGTGACCTGGAGGCTCTTCTTGTGCTGTAGCTGACGTCACATCCACAG 75
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 gtccagctggtctgcaagctggtgaggaagacgtggagctcaagtgaaggtctc 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76 GTGACGCTTGTGCACTGTGAGCTGAGGTGAAGACCTGGGCGCTCAGTGAAGTTTCC 135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 tgcgaagctccgagtcacacatcagatgatctatagctgaggaagacagccct 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 TGCAGGCTTGTGATCTCTTACTTACTAGTTATTTACATACACTGGGTGCGCCAGCCCC 195
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 ggaacagagctcgagtgatgtgagttatataattactatgataatacaaac 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 GGACAAAGCGCTGAGTGGATATATGACCCCTTTCATGCTGATGATATAT 255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 241 cagaagtttaaggaagcaacaaatgacgtgtagaacaagtcgacagcaagcctatcg 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 CAGAAGTTCAAGGCGCAGATCACCATTCACGTAGACACATCCGCGACACAGCTACATG 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 301 gaactgtctcttgagatctgagatacgccgttatattactgtgcaagaagcgctcg 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 316 GAGCTGACACCTGACATCTGAGACACGCGCTGTATTACTGTGCGAGGCGTAAAC 375
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 361 tatatgactactgtgggtcaaggtacacctgttgcagcttcttcta 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 CGCTTGTCTTACTGTGCGCAGGAACCTGCTGACCGCTCTCTCA 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-08-436-717-111
Sequence 111, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE: 536
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 16..420
NAME/KEY: mat_peptide
LOCATION: 16..420
US-08-436-717-111

Query Match      61.3%; Score 248.2; DB 1; Length 433;
Best Local Similarity 75.8%; Pred. No. 8,7e-72;
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Matches: 307:	Conservative	0:	Mismatches	98:	Indels	0:	Gaps	0:
QY	1	atgggttggaactgatactatcttcttcttggtgttaccacaagctcaagggtgtgactctccag	60					
Db	16	ATGGAGCTGACCTGGAGGGCTCTTCTTCTTGTGCTGGCTGTAGCTCCAGGTCTACTCCAG	75					
QY	61	gtccagctggtgcaactcttggggcttgaagtgaaagcctgtagctcagtgaagtgctc	120					
Db	76	GTGCAGCTGTGTGCATCTCTGGAGCTTAGGTGAAGAAGCCTGGGGCCTCAGTAGAGTTTCC	135					
QY	121	tgcaaaagcttcgggtgtacacatcactcgtattatgctatacagtggtgtgagacagctctc	180					
Db	136	TGCAAGCGCTTCTGCACTACTATTCACGTAGTTATATACATCACTGGGTGGCCAGGCCCCC	195					
QY	181	ggacagggccctcagatgtagtattggagtatttaattattctatgataataacaactcaaac	240					
Db	196	GGACCAAGGCTTGTGATGGATGGATATATTTGACCCCTTTCAAAGGTGGTATAGCTATAT	255					
QY	241	cagaagtttaagggaagggccacaatgactgtagaacaagtgcagagacagacacctatgt	300					
Db	256	CAGAAGTTCAGAGGGCAGAGTCAACCATTTACCGTAGACATCCGCCAGCACAGCCTACATG	315					
QY	301	gaacttagtctctttagatcttgaagatacgggcccgttattactgtgcaagtcggccttgg	360					
Db	316	GAGCTGAGCAGCTCTGAGATCTGAAACACACGGCGTGTGTATTACTGTGGCAGAGGGGTAA	375					
QY	361	tatatgacctagtggtgtcaaggtacccctgttcaacgctctccta	405					
Db	376	CGCTTCTCTACTGGGGCCAGGAGACCTGTGACCCGTCTCTCTCA	420					
RESULT								
7								
US-07-634-278-68								
Sequence 68, Application US/07634278								
Patent No. 5530101								
GENERAL INFORMATION:								
APPLICANT: QUEEN, Cary L.								
APPLICANT: CO, Man Sung								
APPLICANT: SCHNEIDER, William P.								
APPLICANT: LANDOLF, Nicholas F.								
APPLICANT: COELINGH, Kathleen L.								
APPLICANT: SELICK, Harold E.								
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS								
NUMBER OF SEQUENCES: 113								
CORRESPONDENCE ADDRESS:								
ADDRESSEE: Townsend and Townsend Khourie and Crew								
STREET: 379 Lytton Avenue								
CITY: Palo Alto								
STATE: California								
COUNTRY: US								
ZIP: 94301								
COMPUTER READABLE FORM:								
MEDIUM TYPE: Floppy disk								
COMPUTER: IBM PC compatible								
OPERATING SYSTEM: PC-DOS/MS-DOS								
SOFTWARE: Patent Release #1.0, Version #1.25								
CURRENT APPLICATION DATA:								
APPLICATION NUMBER: US/07/634,278								
FILING DATE: 19-DEC-1990								
CLASSIFICATION: 424								
PRIOR APPLICATION DATA:								
APPLICATION NUMBER: US 07/590,274								
FILING DATE: 28-SEP-1990								
PRIOR APPLICATION DATA:								
APPLICATION NUMBER: US 07/310,252								
FILING DATE: 13-FEB-1989								
PRIOR APPLICATION DATA:								
APPLICATION NUMBER: US 07/290,975								
FILING DATE: 28-DEC-1988								
ATTORNEY/AGENT INFORMATION:								
NAME: Smith, William M								
REGISTRATION NUMBER: 30,223								
REFERENCE/DOCKET NUMBER: 11823-002600								

```

1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: (415) 326-2400
3 TELEFAX: (415) 326-2422
4 INFORMATION FOR SEQ ID NO: 68:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 405 base pairs
7 TYPE: nucleic acid
8 STRANDEDNESS: single
9 TOPOLOGY: linear
10 MOLECULE TYPE: cDNA
11 FEATURE:
12 NAME/KEY: CDS
13 LOCATION: 1..405
14 US-07-634-278-68
15
16 Query Match 60.5%; Score 245; DB 1; Length 405;
17 Best Local Similarity 75.3%; Pred.No. 9,4e-71;
18 Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
19
20 Oy 1 atgggttggaactgtatcatcttcttcttggttaccacagctcacaggtgtgaactccag 60
21 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
22 1 ATGGGATGGAGCTGGATCTTCTCTCCCTCCGTGAGGAACTGCAGGGCCTCCACTCTGAG 60
23
24 Oy 61 gtccagctggttcagctctggggtcaggtgaagaaagccctgagagctcaagtgatgcc 120
25 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
26 61 GTCCAGCTTTCAGCACTACGAGGACCTGAGCTGGTGAACCTGGGGCTCACTGAAGATATCC 120
27
28 Oy 121 tgcagaagttccgcgtacacattcactgaattatgtctatcacagtgggtgagacaggtcc 180
29 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
30 121 TGCAGAGCTTCTGGATACACATTCTACTGACTACACATGCACTGGGTGAAGCAGACCAT 180
31
32 Oy 181 ggacagggcctcagatgtgattgagttatattactatgatataatacaactaac 240
33 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
34 181 GGAAAGACCTTGAATGGATTGGATATATTTTCTTACAAATGGTGTCTGGCTAACAC 240
35
36 Oy 241 cagaagtttaagggaagccacaatgactgtgagcaagtcgacgacgacgacctatg 300
37 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
38 241 CAGAAGTTTCAAGAGCAAGGCCACATTGACTGTAGACAAATCTCCAGCAGCCTTACATG 300
39
40 Oy 301 gaactagttctcttgagatctgagatacagcgcttattactgtgcgaagacggcctgg 360
41 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
42 301 GACGTCCCGACGCTGACATCTGAGACACTGTGAGACACTGTGACGTATTTACTGTGCAAGAGGGGCGCCCC 360
43
44 Oy 361 tatatgactactgggtgacgaagtacacctgttcacogtctccta 405
45 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
46 361 GCTATGAGACTACTGGGTCAGAGAACCTCAGCACGCTCTCTCA 405
47
48 RESULT 8
49 US-08-477-728-68
50 : Sequence 68, Application US/08477728
51 : Patent No. 5585089
52 : GENERAL INFORMATION:
53 : APPLICANT: QUEEN, Cary L.
54 : APPLICANT: SCHNEIDER, William P.
55 : APPLICANT: SELICK, Harold E.
56 : TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
57 : NUMBER OF SEQUENCES: 113
58 : CORRESPONDENCE ADDRESS:
59 : ADDRESSEE: Townsend and Townsend and Crew LLP
60 : STREET: Two Embarcadero Center, 8th floor
61 : CITY: Palo Alto
62 : STATE: California
63 : COUNTRY: US
64 : ZIP: 94111
65
66 COMPUTER READABLE FORM:
67 MEDIUM TYPE: Floppy disk
68 COMPUTER: IBM PC compatible
69 OPERATING SYSTEM: PC-DOS/MS-DOS
70 SOFTWARE: PatentIn Release #1.0, Version #1.25
71 CURRENT APPLICATION DATA:
72 APPLICATION NUMBER: US/08/477.728

```



OY 241 cagaagtttaagggaagccacaatgactgttagacaagtcgacgagcacagcctataty 300  
|||||  
Db 241 CAGAAGTTCAAGACCAAGCCACATTGACTGTAGACAATTCCTCCAGCAGACGCTACATG 300  
OY 301 gaacttgcttcttgagctcgtgagatagcgccgtttattctctgtcgaagcgccg 360  
|||||  
Db 301 GAGCTCCGACCGCTGACACTGTGAGACTCTGCAGCTATTACTGTGCAAGAGGGGCCCC 360  
OY 361 tataatgactctgggtgcaaggtacccctgtcacgcgtctctca 405  
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Db 361 GCTATGAGCTACTGGGCTCAAGAACCTGCAGTCAACGCTCTCTCA 405

RESULT 10  
US-08-487-200-68  
Sequence 68, Application US/08487200  
Patent No. 5693762  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..405  
US-08-487-200-68

Query Match 60.5%; Score 245; DB 1; Length 405;  
Best Local Similarity 75.3%; Pred. No. 9.4e-71;  
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

OY 1 atggatggaactgtatcatcttcttctgtgttaccacagctagatgtgactccag 60  
|||||  
Db 1 ATGGATGGAGCTGGATCTTCTCTCCCTGTCAGGAACCTGCAGGCGTCCACTCTGAG 60  
OY 61 gtccagctggtgcaactctcgggctgagtgaaagacgttggaagctgaagtgtgccc 120  
|||||  
Db 61 GTCCAGCTTCAAGCTCAAGGACCTGAGCTGCTGGAACCTGGGCGCTCAAGATATATCC 120  
OY 121 tgcagaagcttcgcggtacacattcactgattatgtctatcacagtgggtgagacgctct 180  
|||||  
Db 121 TGCAAGGCTTCTGGATGATACATCTGACTGACATGACATGACACTGGGTGAGAGGCCAT 180  
OY 181 ggcagagcgctcagatgagtgagttatataattactatgataatacaactacaac 240  
|||||  
Db 181 GGAAGAGCGCTTGAAGTGAATGATATATTATCTTCAATGCTGATGCTACTGCTACAAAC 240  
OY 241 cagaagtttaagggaagccacaatgactgttagacaagtcgacgagcacagcctataty 300  
|||||  
Db 241 CAGAAGTTCAAGACCAAGCCACATTGACTGTAGACAATTCCTCCAGCAGACGCTACATG 300  
OY 301 gaacttgcttcttgagctcgtgagatagcgccgtttattctctgtcgaagcgccg 360  
|||||  
Db 301 GAGCTCCGACCGCTGACACTGTGAGACTCTGCAGCTATTACTGTGCAAGAGGGGCCCC 360  
OY 361 tataatgactctgggtgcaaggtacccctgtcacgcgtctctca 405  
|||||  
Db 361 GCTATGAGCTACTGGGCTCAAGAACCTGCAGTCAACGCTCTCTCA 405

RESULT 11  
US-08-484-537-68  
Sequence 68, Application US/08484537  
Patent No. 6180370  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:



```

1  APPLICANT: CO, Man Sung
2  APPLICANT: SCHNEIDER, William P.
3  APPLICANT: LANDOLFI, Nicholas F.
4  APPLICANT: COELINGH, Kathleen L.
5  APPLICANT: SELICK, Harold E.
6  TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
7  NUMBER OF SEQUENCES: 113
8  CORRESPONDENCE ADDRESS:
9  ADDRESS: Townsend and Townsend Kourie and Crew
10 STREET: 379 Lytton Avenue
11 CITY: Palo Alto
12 STATE: California
13 COUNTRY: US
14 ZIP: 94301
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.25
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/07/634,278
24 FILING DATE: 19-DEC-1990
25 CLASSIFICATION: 424
26
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/590,274
29 FILING DATE: 28-SEP-1990
30
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 07/310,252
33 FILING DATE: 13-FEB-1989
34
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: US 07/290,975
37 FILING DATE: 28-DEC-1988
38
39 ATTORNEY/AGENT INFORMATION:
40 NAME: Smith, William M
41 REGISTRATION NUMBER: 30,223
42 REFERENCE/DOCKET NUMBER: 11823-002600
43 TELECOMMUNICATION INFORMATION:
44 TELEPHONE: (415) 326-2400
45 TELEFAX: (415) 326-2422
46
47 INFORMATION FOR SEQ ID NO: 18:
48 SEQUENCE CHARACTERISTICS:
49 LENGTH: 433 base pairs
50 TYPE: nucleic acid
51 STRANDEDNESS: single
52 TOPOLOGY: linear
53 MOLECULE TYPE: DNA
54 HYPOTHETICAL: NO
55 FEATURE:
56 NAME/KEY: CDS
57 LOCATION: 6..410
58 OTHER INFORMATION: /product= "Humanized anti-Tac heavy
59 OTHER INFORMATION: chain variable region", Seq ID. 19"
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Db	6 ATGGGATGAGCTGGATCTTCTCTCCCTCGTAGGATACCGGGGGCTGCACCTCTCAG	65		
OY	61 gtccagcccggtgtgcactctctggggctgaagttgaagaagccctgggagctcagctgaagtgctcc	120		
Db	66 GTCCAGCTTGTCACATCTCGGGGCTGAAGCAGAAACCTGCTCGAGCTGAAGGCTTCC	125		
OY	121 tgcgaagcttcgggtgtaccatcactgcgtatgaatgtcatcagttgggtggagaagctcct	180		
Db	126 TGCAAGGCTTCTGGCTACACCTTACTACCTACAGAGATGCACTGGTAAAGCAGGCCCTT	185		
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1 RESULT 14
2 US-08-477-728-18
3 : Sequence 18, Application US/08477728
4 : Patent No. 5585089
5 : GENERAL INFORMATION:
6 :
7 : APPLICANT: QUEEN, Cary L.
8 : APPLICANT: SCHNIEDER, William P.
9 : APPLICANT: SELICK, Harold E.
10 : TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
11 : NUMBER OF SEQUENCES: 113
12 : CORRESPONDENCE ADDRESS:
13 : ADDRESSEE: Townsend and Townsend and Crew LLP
14 : STREET: Two Embarcadero Center, 8th Floor
15 : CITY: Palo Alto
16 : STATE: California
17 : COUNTRY: US
18 : ZIP: 94111
19 :
20 : COMPUTER READABLE FORM:
21 : MEDIUM TYPE: Floppy disk
22 : COMPUTER: IBM PC compatible
23 : OPERATING SYSTEM: PC-DOS/MS-DOS
24 : SOFTWARE: Patentin Release #1.0, Version #1.25
25 : CURRENT APPLICATION DATA:
26 : APPLICATION NUMBER: US/08/477,728
27 : FILING DATE: 07-JUN-1995
28 : CLASSIFICATION: 424
29 :
30 : PRIOR APPLICATION DATA:
31 : APPLICATION NUMBER: US 07/634,278
32 : FILING DATE: 19-DEC-1990
33 : PRIOR APPLICATION DATA:
34 : APPLICATION NUMBER: US 07/590,274
35 : FILING DATE: 28-SEP-1990
36 :
37 : PRIOR APPLICATION DATA:
38 : APPLICATION NUMBER: US 07/310,252
39 : FILING DATE: 13-FEB-1989
40 : PRIOR APPLICATION DATA:
41 : APPLICATION NUMBER: US 07/290,975
42 : FILING DATE: 28-DEC-1988
43 : ATTORNEY/AGENT INFORMATION:
44 : NAME: Smith, William M
45 : REGISTRATION NUMBER: 30,223
46 : REFERENCE/DOCKET NUMBER: 11823-002600
47 : TELECOMMUNICATION INFORMATION:
48 : TELEPHONE: (415) 326-2400
49 : TELEFAX: (415) 326-2422
50 : INFORMATION FOR SEQ ID NO: 18:
51 : SEQUENCE CHARACTERISTICS:
52 : LENGTH: 433 base pairs
53 : TYPE: nucleic acid
54 : STRANDEDNESS: single
55 : TOPOLOGY: linear
56 : MOLECULE TYPE: DNA
57 : HYPOTHETICAL: NO
58 : FEATURE:
59 : NAME/KEY: CDS
60 : LOCATION: 6..410
61 : OTHER INFORMATION: /product= "Humanized anti-Tac heavy
62 : chain variable region, Seq ID. 19"

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US-08-477-728-18

Query Match 58.9%; Score 238.6; DB 1; Length 433;  
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Matches 301; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1 atgggttggaacgtatcatctcttcttctgttaccacagctaaagtggtactccag 60  
DB 6 ATGGGATGAGAGCTGATCTTCTCTCTCTCTCTGACAGGTACCGGGCGGTCTCTCAG 65  
QY 61 gtccagcttggtgagctggtgagctggaagctggagctcagtcagtaagtgctc 120  
DB 66 GTCCAGCTTGCTGAGTCTGGGGCTGAAGTCAAGAACTGCTGAGCGTGAAGGTCTCC 125  
QY 121 tgcgaagcttcgagctacacatcactgattatgctacagtggtgagacagctctc 180  
DB 126 TGCAGAGCTTCTGGCTACACTTACTAGCTACAGATGCACTGGGTATCTGAAATACAT 185  
QY 181 ggacagggcctcgagtgagtgagttatataattactatgataatacaactacaac 240  
DB 186 GGACAGGCTCTGGAATGATGATATATATATATATATATATATATATATATATATAT 245  
QY 241 cagaagcttgaagcgaagcgaacatgactgtagaacaagtcgacgagcagcctatag 300  
DB 246 CAGAGGTTCAAGGACAGGCAACAAATTAATGACAGAGATGCAATACCAATATACATG 305  
QY 301 gaacttgcttcttgagatctgagagatagcgcttattactgtgcaagagcgctctg 360  
DB 306 GAAGTGAAGACCCGTGAATCTGAGAGACCCGCACTTATCTGTGCAAGAGGGGGGGG 365  
QY 361 tatatgactactggtggtcgaagtagccttgtagccgtctctca 405  
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RESULT 15

US-08-474-040-18  
Sequence 18, Application US/08474040  
Patent No. 5693761  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 433 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 6..410  
OTHER INFORMATION: /product= "Humanized anti-Tac heavy  
OTHER INFORMATION: chain variable region, Seq ID. 19"

US-08-474-040-18

Query Match 58.9%; Score 238.6; DB 1; Length 433;  
Best Local Similarity 74.3%; Pred. No. 1,2e-68;  
Matches 301; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1 atgggttggaacgtatcatctcttcttctgttaccacagctaaagtggtactccag 60  
DB 6 ATGGGATGAGAGCTGATCTTCTCTCTCTCTGACAGGTACCGGGCGGTCTCTCAG 65  
QY 61 gtccagcttggtgagctggtgagctggaagctggagctcagtcagtaagtgctc 120  
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QY 181 ggacagggcctcgagtgagtgagttatataattactatgataatacaactacaac 240  
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QY 361 tatatgactactggtggtcgaagtagccttgtagccgtctctca 405  
DB 366 GTCTTTGACTACTGGGGCCAGGAACCTGTGTACAGTCTCTCA 410

Search completed: August 26, 2002, 16:14:58  
Job time: 4247 sec



Mon Aug 26 17:25:46 2002

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Page 11





A:Reference number: A02042; MUID:82222262  
 A:Accession: A02042  
 A:Molecule type: mRNA  
 A:Residues: 1-136 <RNA>  
 A:Cross-references: GB:J00494; NID:g195010; PIDN:AAA38130.1; PID:g195011  
 A>Note: the sequence was determined from the differentiated gene  
 C:Genetics:  
 A:Intons: 16/1  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; Immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-115/Product: Ig heavy chain V region (BCL1) #status predicted <MAY>  
 F:34-117/Domain: Immunoglobulin homology <IMM>

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 Matches 99; Conservative 14; Mismatches 23; Indels 1; Gaps 1;  
 QY 1 MGWNCIFFLVTTATGVHSQVQLVQSGAEVKKPGSSSVKSCASGYFTFDYAIQWVROAP 60  
 DB 1 MGWNCIFFLVTTATGVHSQVQLVQSGAEVKKPGSSSVKSCASGYFTFDYAIQWVROAP 60  
 QY 61 GQGLEWIGVNIYYDNTNINQKFKGKATMYDKSTSTAYMELSLRSDTAIVYICAR-AA 119  
 DB 61 AKSLEWIGVISTYNGNTSYNOKFKGKATMYDKSSSTVHMLARLTSDESNLYCARYG 120  
 QY 120 WYMDYWGQGLTVTVSS 135  
 DB 121 NYFDYWGQGLTVTVSS 136

RESULT 3  
 E32513  
 Ig heavy chain precursor V region (MRL22) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 23-Jul-1999  
 C:Accession: E32513  
 R:Kofler, R.; Strohal, R.; Balders, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;  
 J. Clin. Invest. 82, 852-860, 1988  
 A:Title: Immunoglobulin kappa light chain variable region gene complex organization and  
 A:Reference number: A94689; MUID:88331394  
 A:Accession: E32513  
 A:Molecule type: DNA  
 A:Residues: 1-138 <KOF>  
 A:Cross-references: GB:M20835; NID:g196945; PIDN:AAA38847.1; PID:g196946  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; Immunoglobulin  
 F:34-117/Domain: Immunoglobulin homology <IMM>

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 Matches 101; Conservative 13; Mismatches 19; Indels 7; Gaps 3;  
 QY 1 MGWNCIFFLVTTATGVHSQVQLVQSGAEVKKPGSSSVKSCASGYFTFDYAIQWVROAP 60  
 DB 1 MGWNCIFFLVTTATGVHSQVQLVQSGAEVKKPGSSSVKSCASGYFTFDYAIQWVROAP 60  
 QY 61 GQGLEWIGVNIYYDNTNINQKFKGKATMYDKSTSTAYMELSLRSDTAIVYICARA 118  
 DB 61 GQGLEWIG--NIPGSSSTNNEKFKSKATLVTSSSTAYMOLSLSDSAVYICAR 118  
 QY 119 A---WYMDYWGQGLTVTVSS 135  
 DB 119 LRYRYAMDYWGQGLTVTVSS 138

RESULT 4  
 S49530  
 anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 01-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 23-Jul-1999

C:Accession: S49530  
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.  
 A:Reference number: S48797  
 A:Accession: S49530  
 A>Status: preliminary  
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 F:34-117/Domain: Immunoglobulin homology <IMM>

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 Matches 101; Conservative 7; Mismatches 27; Indels 0; Gaps 0;  
 QY 1 MGWNCIFFLVTTATGVHSQVQLVQSGAEVKKPGSSSVKSCASGYFTFDYAIQWVROAP 60  
 DB 1 MDWTMRILFLVAAATGVHSQVQLVQSGAEVKKPGASVSKSCASGYFTGYMHVROAP 60  
 QY 61 GQGLEWIGVNIYYDNTNINQKFKGKATMYDKSTSTAYMELSLRSDTAIVYICARA-AW 120  
 DB 61 GQGLEWIGVNIYYDNTNINQKFKGKATMYDKSTSTAYMELSLRSDTAIVYICARA-AW 120  
 QY 121 YMDYWGQGLTVTVSS 135  
 DB 121 GYNTYWGQGLTVTVSS 135

RESULT 5  
 A30577  
 Ig heavy chain precursor V region (MRL10) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 04-May-1989 #sequence\_revision 04-May-1989 #text\_change 16-Aug-1996  
 C:Accession: A30577  
 R:Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Th  
 J. Exp. Med. 161, 805-815, 1985  
 A:Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely r  
 A:Reference number: A30577; MUID:85159423  
 A:Accession: A30577  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-135 <KOF>  
 A:Cross-references: GB:M37621  
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
 C:Keywords: heterotrimer; Immunoglobulin  
 F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match 70.8%; Score 510; DB 2; Length 135;  
 Best Local Similarity 72.3%; Pred. No. 1.6e-37;  
 Matches 99; Conservative 13; Mismatches 21; Indels 4; Gaps 2;  
 QY 1 MGWNCIFFLVTTATGVHSQVQLVQSGAEVKKPGSSSVKSCASGYFTFDYAIQWVROAP 60  
 DB 1 MGWNCIFFLVTTATGVHSQVQLVQSGAEVKKPGASVSKSCASGYFTSYIMWVROAP 60  
 QY 61 GQGLEWIGVNIYYDNTNINQKFKGKATMYDKSTSTAYMELSLRSDTAIVYICARA 118  
 DB 61 GQGLEWIG--NIPGSSSTNNEKFKSKATLVTSSSTAYMOLSLSDSAVYICARL 118  
 QY 119 AWYMDYWGQGLTVTVSS 135  
 DB 119 VGCPAYWGQGLTVTVSA 135

RESULT 6  
 MHM518  
 Ig heavy chain precursor V region (B1-8) - mouse  
 N:Contains: Ig heavy chain precursor V region 186-2  
 C:Species: Mus musculus (house mouse)

```
Query Match          69.4%; Score 500; DB 2; Length 139;
Best Local Similarity 68.3%; Pred. No. 1,2e-36;
Matches 95; Conservative 19; Mismatches 21; Indels 4; Gaps 1;
```

OY    1 MGMCNCTIFLVTATGAVSOVQVLVSOGAEVKKPGGSVAVCCKASGYTFTDYAIOVRAP 60  
| | | | : | | | : | | | | | | : | | | | | | | | | | | : | | |  
Db    1 MGWSWTFLELLTGAGVISEVOLOQGPELVKPGCASVMSCASKASYRTTDYMHVAKSN 60

OY    61 GGCELMICIVNIYYDNTNYNOKFKGATMFDKSTAYMETSLRSEDFAVVYCARRAM 120  
| : | | | | | | | : | | | | | | | | | | | | | | | | | | | : :  
Db    61 GKSELMICYINPYNDYTYSNOFKGKATLTVDKSSSTAQMQLNSLTSDSAVIYCARISY 120

OY    121 Y----MDYWGCGTLTVSS 135  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db    121 YSYAMDYGCGTGVTVSS 139

RESULT         8  
JL0076  
Ig heavy chain precursor V region (anti-phenylloxalone, 18C10) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
C:Accession: JI0076  
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.  
Mol. Immunol. 25, 859-865, 1988  
A>Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive B-cell epitopes  
F:Reference number: JL0076; MUID:89096973  
A:Accession: JI0076  
A:Molecule type: mRNA  
A:Residues: 1-141 <KAA>  
A:Cross-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PTD:g195852  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Dominant signal sequence #stratus predicted <SIG>  
F:20-141/Product: Ig heavy chain #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMH>  
F:50-54/Region: complementarity-determining 1  
F:69-85/Region: complementarity-determining 2  
F:123-135/Region: J2 segment  
F:136-141/Region: C

Query Match  
Best Local Similarity 69.2%; Score 498; DB 2; Length 141;  
Matches 94; Conservative % 15; Mismatches 26; Indels 0; Gaps 0;

OY    1 MGMCNCTIFLVTATGAVSOVQVLVSOGAEVKKPGGSVAVCCKASGYTFTDYAIOVRAP 60  
| | | | : | | | : | | | | | | : | | | | | | | | | | | : | | |  
Db    1 MGWSCIMFLFATATGAVSHSQVOLQPGAELVKPGASVMSLKASCASYRTTSYMMHVAKORP 60

OY    61 GGCELMICIVNIYYDNTNYNOKFKGATMFDKSTAYMETSLRSEDFAVVYCARRAM 120  
| : | | | | | | | : | | | | | | | | | | | | | | | | | | | : :  
Db    61 GRGLEMICRIDPNSGGITVNEFKSKATLTVDKPSSTAIMQLSLSDEDSAVIYCARGP 120

OY    121 YMDYWGCGTLTVSS 135  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db    121 AGDYWGCGTTLTVSS 135

RESULT         9  
A32483  
Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 16-Aug-1996  
C:Accession: A32483  
R:Lairick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck  
J.Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989  
A>Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells  
F:Reference number: A32483; MUID:89273586  
A:Accession: A32483  
A>Status: preliminary



Cell 24, 625-637, 1981  
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: some  
A:Reference number: A90809; M01D:81234548  
A:Accession: A02038  
A:Molecule type: mRNA  
A:Residues: 1-137 <BOT>  
A:Cross-references: GB:000539; NID:g195118; PID:AAA38172.1; PID:g195119  
A>Note: the gamma-2a chain mRNA was cloned from a hybridoma making antibodies to the hap  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-137/Product: Ig heavy chain V region (S43) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:118-122/Region: D segment  
F:123-137/Region: J segment (JH2)







Qy 120 WYMDYWGOGTLTVSS 135  
 Db 121 NYFDYWGOGTLTVSS 136

RESULT 2

HV07\_MOUSE STANDARD; PRT; 139 AA.  
 ID HV07\_MOUSE  
 AC P01751; P01752;  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 19 heavy chain V region B1-8/186-2 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
 CC (NPB ANTIBODIES).  
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 CC -----  
 CC EMBL: J00529; AAA38170.1; -  
 CC PIR: A02034; MIMIS18.  
 CC InterPro: IPR003006; Ig\_MHC.  
 CC Pfam: PF00047; Ig\_V.  
 CC SMART: SM00406; IgV\_1.  
 CC KMW Immunoglobulin V region; Signal.  
 CC FT SIGNAL 1 19  
 CC FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.  
 CC FT DOMAIN 20 49 FRAMEWORK-1.  
 CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 CC FT DOMAIN 55 68 FRAMEWORK-2.  
 CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 CC FT DOMAIN 86 117 FRAMEWORK-3.  
 CC FT DOMAIN 118 124 D SEGMENT.  
 CC FT DISULFID 41 135 JH2 SEGMENT.  
 CC FT NON\_TER 137 137 BY SIMILARITY.  
 CC FT SEQUENCE 139 AA; 15419 MW; 1B57D4FDC9F465 CRC64;

Query Match 69.6%; Score 501; DB 1; Length 139;  
 Best Local Similarity 68.3%; Pred. No. 1.4e-43;  
 Matches 95; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

Qy 1 MGNCIIFLVATATGVSVOLOVSGAEVKKPGSSVYKSCASGYFTFYAIQWVQAP 60  
 Db 1 MGNSCIMLFPLAATATGVSVOLOVSGAEVKKPGASVYKSCASGYFTFYLMHWVQAP 60  
 Qy 61 GGGLEWIGVINYDNTNYNQKFKGKATMTVDKSTFAYMELSLRSEDYAVYYCA--RA 117  
 Db 61 GRGLEWIGRIDPNVSGGTYVHFRSKATLTITDKPSSFAYMQLSLTSEDSAVYYCARYL 120  
 Qy 118 -AAYMDYWGOGTLTVSS 135  
 Db 121 NYFDYWGOGTLTVSS 136

Db 121 YGSSYFDYWGOGTLTVSS 139

RESULT 3

HV11\_MOUSE STANDARD; PRT; 137 AA.  
 ID HV11\_MOUSE  
 AC P01755;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 19 heavy chain V region S43 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
 CC (NPB ANTIBODIES).  
 CC -----  
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 CC -----  
 CC EMBL: J00539; AAA38172.1; -  
 CC PIR: A02038; GZMS43.  
 CC InterPro: IPR003006; Ig\_MHC.  
 CC Pfam: PF00047; Ig\_V.  
 CC SMART: SM00406; IgV\_1.  
 CC KMW Immunoglobulin V region; Signal.  
 CC FT SIGNAL 1 19  
 CC FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.  
 CC FT DOMAIN 20 49 FRAMEWORK-1.  
 CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 CC FT DOMAIN 55 68 FRAMEWORK-2.  
 CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 CC FT DOMAIN 86 117 FRAMEWORK-3.  
 CC FT DOMAIN 118 122 D SEGMENT.  
 CC FT DISULFID 41 135 JH2 SEGMENT.  
 CC FT NON\_TER 137 137 BY SIMILARITY.  
 CC FT SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8BC9 CRC64;

Query Match 67.8%; Score 488; DB 1; Length 137;  
 Best Local Similarity 67.2%; Pred. No. 2.7e-42;  
 Matches 92; Conservative 15; Mismatches 28; Indels 2; Gaps 1;

Qy 1 MGNCIIFLVATATGVSVOLOVSGAEVKKPGSSVYKSCASGYFTFYAIQWVQAP 60  
 Db 1 MGNSCIMLFPLAATATGVSVOLOVSGAEVKKPGASVYKSCASGYFTFYLMHWVQAP 60  
 Qy 61 GGGLEWIGVINYDNTNYNQKFKGKATMTVDKSTFAYMELSLRSEDYAVYYCA--RA 118  
 Db 61 GRGLEWIGRIDPNVSGGTYVHFRSKATLTITDKPSSFAYMQLSLTSEDSAVYYCARYL 120  
 Qy 119 AAYMDYWGOGTLTVSS 135  
 Db 121 NYFDYWGOGTLTVSS 136

AC	DT	23-OCT-1986	(Rel. 02, Created)
AC	DT	23-OCT-1986 <td>(Rel. 02, Last sequence update)</td>	(Rel. 02, Last sequence update)
DT	DT	21-JUL-1986 <td>(Rel. 01, Last sequence update)</td>	(Rel. 01, Last sequence update)
DE	DE	15-JUL-1999 <td>(Rel. 38, Last annotation update)</td>	(Rel. 38, Last annotation update)
OS	OS	mus musculus (Mouse)	
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	OX	NCBI_TaxID=10090;	
RN	RN	SEQUENCE FROM N.A.	
RP	RP	Medline=84248078; PubMed=6429663;	
RA	RA	Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,	
RT	RT	Tucker P.W.,	
RL	RL	delta in an Igd-secreting plasmacytoma,	
DR	DR	Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).	
DR	DR	PIR: A02033; HVMST7.	
DR	DR	InterPro: IPR003006; IG_MHC.	
DR	DR	InterPro: IPR003596; IG_V.	
DR	DR	Pfam: PF00047; Ig_1.	
DR	DR	SMART: SM00406; Igv_1.	
KW	KW	Immunoglobulin V region; Signal.	
FT	FT	SIGNAL	1
FT	FT	CHAIN	21
FT	FT	DOMAIN	21
FT	FT	DOMAIN	50
FT	FT	DOMAIN	55
FT	FT	DOMAIN	69
FT	FT	DOMAIN	86
FT	FT	DOMAIN	118
FT	FT	DOMAIN	128
FT	FT	DISULFID	41
FT	FT	NON TER	138
SQ	SQ	SEQUENCE	138 AA; 15576 MW; 748137E4C6907B8E CRC64;
Query Match	Best Local Similarity	67.7%; Score 487.5; DB 1; Length 138;	
Matches	95; Conservative	16; Mismatches 24; Indels 3; Gaps 1	
OY	OY	1 MGNMCIIFLYTTATGHSVOVLVSQAEVKKPGSSVKVSKCAGYTFDYAIQWVRQAP 60	
DB	DB	1 MGNMCIIFLYTTATGHSVOVLVSQAEVKKPGSSVKVSKCAGYTFDYAIQWVRQAP 60	
OY	OY	61 GGGLEMIIVINYYNTYVNOKEFKGATPVDRKSTAVNMLSSLRSEPTAYYYCARAA 120	
DB	DB	61 GGGLEMIIVINYYNTYVNOKEFKGATPVDRKSTAVNMLSSLRSEPTAYYYCARAA 120	
OY	OY	121 YMD--YWGQGLTVVSS 135	
DB	DB	121 YMD--YWGQGLTVVSS 135	
RESULT	5		
HV02_MOUSE	HV02_MOUSE	STANDARD;	PRT; 140 AA.
ID	ID	P01746;	
DT	DT	21-JUL-1986 (Rel. 01, Created)	
DT	DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	DT	15-JUL-1999 (Rel. 38, Last annotation update)	
DE	DE	Ig heavy chain V region 9367 precursor.	
OS	OS	Mus musculus (Mouse).	
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	OX	NCBI_TaxID=10090;	
RN	RN	SEQUENCE FROM N.A.	
RP	RP	STRAIN-A/J;	
RX	RX	Medline=82152818; PubMed=6801765;	

RA	Slms J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA	Capra J.D.,
RT	"Somatic mutation in genes for the variable portion of the
RT	Immunoglobulin heavy chain."
RL	Science 216:309-311(1982).
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; J00493; AAA38128.1; -.
DR	PIR; A02028; HVMMSG7.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; Igv; 1.
FW	Immunoglobulin v region; Antiarsenate antibody; Hybridoma; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT	NON_TER 140 140
SQ	SEQUENCE 140 AA: 15514 MW: 25A4CBBE31DA5C88 CRC64:

	Query Match	67.2%	Score 483.5;	DB 1;	Length 140;
	Best Local Similarity	65.7%;	Pred. No. 7.9e-42;		
	Matches 92;	Conservative 17;	Mismatches 26;	Indels 5;	Gaps 1;
OY	1 MGNMCIIFELVTATGVSQVOLVSGAEVKKPGSSSVSCASAGTPTDAIQWROAP 60           :           :                   Db 1 MGMSFIPLFLISYAGVAHSEVOLOQSAGEIVLRAGSSVASCKASYTTTSIGINNVKR P 60  OY 61 GGGLEWICVIINYDNTNIYNOKFEKGATMTVDKSTGYAMELSSRLRSDTAIVYYCARAA W 120           :     :           :                                   Db 61 GGGEWMETIYINPBGNGIYINNEKFEGKTTLTVDKSSSTAYMWOLRLSLTSDSAVYFCARSH Y 120  OY 121 Y-----MDYWGOGTLVITYSS 135                 Db 121 YGSTIDEDYWGOGTPILVSS 140  RESULT 6 HY06_MOUSE . STANDARD; PRF: 117 AA. ID HY06_MOUSE . AC P01750; DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last sequence update) DE 15-JUL-1999 (Rel. 38, Last annotation update) DE IG heavy chain V region 102 precursor. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxID=10090; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=C57BL/6; RX MEDLINE=81234548; PubMed=6788376; RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., RA Baltimore D.; RT "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981). CC -! MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES. DR PIR: A02032; HVMS02. DR InterPro: IPRO03006; Ig_MHC. DR InterPro: IPRO03596; Ig_V. DR Pfam: PF00047; Ig_1. DR SMART: SM00406; IGV_1. KW Immunoglobulin V region; Signal.				

FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 102.  
 FT CHAIN 20 117 FRAMEWORK-1.  
 FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 69 85 FRAMEWORK-3.  
 FT DISULFID 86 117 BY SIMILARITY.  
 FT NON\_TER 41 115  
 FT SEQUENCE 117 AA: 12867 MW: 740A65DD851FCA8C CRC64;

Query Match 65.3%; Score 470; DB 1; Length 117;  
 Best Local Similarity 76.7%; Pred. No. 1.5e-40;  
 Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGNWCIIFLVTTATGVSQVQVLSGAEVKKRGSSVKYKSCASGTYTDTAIAQWVQAP 60  
 DB 1 MGNWCIIFLVTTATGVSQVQVLSGAEVKKRGSSVKYKSCASGTYTDTAIAQWVQAP 60  
 QY 61 GGGLEWIGVINIYDNTNOKFKGATVTDKSTSTAVMELSLSEDTAVYYCAR 116  
 DB 61 GGGLEWIGVINIYDNTNOKFKGATVTDKSTSTAVMELSLSEDTAVYYCAR 116

RESULT 7  
 HV05\_MOUSE STANDARD; PRT: 117 AA.

AC P01749; 21-JUL-1986 (rel. 01, Created)  
 DT 21-JUL-1986 (rel. 01, Last sequence update)  
 DT 15-JUL-1999 (rel. 38, Last annotation update)  
 DE Ig heavy chain V region 3 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Karl T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
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 CC -----  
 CC EMBL: J00536; AAA38605.1; -;  
 DR PIR: A02031; HVMS3  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117

SO SEQUENCE 117 AA: 13016 MW: 427C861C53975EDC CRC64;

Query Match 64.3%; Score 463; DB 1; Length 117;  
 Best Local Similarity 75.6%; Pred. No. 7.4e-40;  
 Matches 90; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 1 MGNWCIIFLVTTATGVSQVQVLSGAEVKKRGSSVKYKSCASGTYTDTAIAQWVQAP 60  
 DB 1 MGNWCIIFLVTTATGVSQVQVLSGAEVKKRGSSVKYKSCASGTYTDTAIAQWVQAP 60  
 QY 61 GGGLEWIGVINIYDNTNOKFKGATVTDKSTSTAVMELSLSEDTAVYYCAR 117  
 DB 61 GGGLEWIGVINIYDNTNOKFKGATVTDKSTSTAVMELSLSEDTAVYYCAR 117

RESULT 8  
 HV04\_MOUSE STANDARD; PRT: 117 AA.

AC P01748; 21-JUL-1986 (rel. 01, Created)  
 DT 21-JUL-1986 (rel. 01, Last sequence update)  
 DT 15-JUL-1999 (rel. 38, Last annotation update)  
 DE Ig heavy chain V region 23 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Karl T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
 CC -----  
 CC PIR: A02030; HVMS23  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.  
 FT DOMAIN 20 49 FRAMEWORK-1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 55 68 FRAMEWORK-2.  
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 86 117 FRAMEWORK-3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SO SEQUENCE 117 AA: 12772 MW: C530F829C906F69B CRC64;

Query Match 62.1%; Score 447; DB 1; Length 117;  
 Best Local Similarity 71.8%; Pred. No. 3e-38;  
 Matches 84; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MGNWCIIFLVTTATGVSQVQVLSGAEVKKRGSSVKYKSCASGTYTDTAIAQWVQAP 60  
 DB 1 MGNWCIIFLVTTATGVSQVQVLSGAEVKKRGSSVKYKSCASGTYTDTAIAQWVQAP 60  
 QY 61 GGGLEWIGVINIYDNTNOKFKGATVTDKSTSTAVMELSLSEDTAVYYCAR 117  
 DB 61 GGGLEWIGVINIYDNTNOKFKGATVTDKSTSTAVMELSLSEDTAVYYCAR 117

RESULT 9  
 HV1B\_HUMAN STANDARD; PRT: 117 AA.



```

FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;
```

```

Query Match 61.0%; Score 439; DB 1; Length 117;
Best Local Similarity 70.1%; Pred. No. 1.9e-37;
Matches 82; Conservative 14; Mismatches 21; Indels 0; Gaps 0;
```

```

OY 1 MGNMNCIIFLVTTATGVSQVQVDSGAEVKKRGSSVSKVSCASGYTFTDYAIQWYCAR 60
DB 1 MGNMNCIIFLVTTATGVSQVQVDSGAEVKKRGSSVSKVSCASGYTFTSYMHWKORP 60
OY 61 GQGLEWIGVINIYDNTNOKFKGKATMTVDKSTSTAVMELSLSEDTAVYYCAR 117
DB 61 GQGLEWIGRIDPNSGGTKYNEKFKSKATLTVDPSSTAYMQLSLTSEDSAVYYCAR 117
```

## RESULT 12

```

ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.O.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus";
RL EMBO J. 7:1047-1051(1988).
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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```

```

Query Match 61.0%; Score 439; DB 1; Length 117;
Best Local Similarity 73.5%; Pred. No. 1.9e-37;
Matches 86; Conservative 6; Mismatches 25; Indels 0; Gaps 0;
```

```

OY 1 MGNMNCIIFLVTTATGVSQVQVDSGAEVKKRGSSVSKVSCASGYTFTDYAIQWYCAR 60
DB 1 MGNMNCIIFLVTTATGVSQVQVDSGAEVKKRGSSVSKVSCASGYTFTGYMHWKORP 60
```

```

OY 61 GQGLEWIGVINIYDNTNOKFKGKATMTVDKSTSTAVMELSLSEDTAVYYCAR 117
DB 61 GQGLEWIGRIDPNSGGTKYNEKFKSKATLTVDPSSTAYMQLSLTSEDSAVYYCAR 117
```

```

RESULT 13
HV49_MOUSE STANDARD; PRT; 117 AA.
ID HV49_MOUSE
AC P06328;
```

```

DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D.; Alt F.W.;
RT "developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@sib.ch).
```

```

Query Match 60.4%; Score 435; DB 1; Length 117;
Best Local Similarity 69.2%; Pred. No. 4.8e-37;
Matches 81; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
```

```

OY 1 MGNMNCIIFLVTTATGVSQVQVDSGAEVKKRGSSVSKVSCASGYTFTDYAIQWYCAR 60
DB 1 MGNMNCIIFLVTTATGVSQVQVDSGAEVKKRGSSVSKVSCASGYTFTSYMHWKORP 60
OY 61 GQGLEWIGVINIYDNTNOKFKGKATMTVDKSTSTAVMELSLSEDTAVYYCAR 117
DB 61 GQGLEWIGRIDPNSGGTKYNEKFKSKATLTVDPSSTAYMQLSLTSEDSAVYYCTR 117
```

```

RESULT 14
HV10_MOUSE STANDARD; PRT; 117 AA.
ID HV10_MOUSE
AC P01754; P11270;
```

```

DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region I45 precursor.
```









ID	AC	PRELIMINARY:	PRT:	473 AA.
DT	09DBL4			
DT	01-JUN-2001 (TEMBLrel. 17, Created)			
DT	01-JUN-2001 (TEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)			
DE	1810060009RIK PROTEIN.			
GN	IGH-1 OR 1810060009RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-C57BL/6J; TISSUE=PANCREAS;			
RX	MEDLINE=210855660; PubMed=11217851;			
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Atakawa T., Hata A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kodori C., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Glassi C., King B., Koehli A.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schirrm L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Glusichluc S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombearts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitteker G., Wilmink L.,			
RA	Wyshnaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
DR	EMBL; AK007918; BAB2549.1; -.			
DR	HSSP; P01842; 7FAB.			
DR	MGD; MGI:96443; Igh-1.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR003597; Ig_c1.			
DR	InterPro; IPR003600; Ig_like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 4.			
DR	SMART; SM00409; Ig; 2.			
DR	SMART; SM00407; IGC1; 3.			
DR	SMART; SM00406; IGV; 1.			
DR	SMART; SM00410; IGLike; 1.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN.1.			
QO	SEQUENCE 473 AA; 51699 MW; 9DED57541475FBB CRC64;			

[illegible]

DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE HYPOTHETICAL 53.0 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N/A.  
RC TISSUE=KIDNEY; |  
RC Strausberg R.; |  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC013539; AANH3539.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match	65.8%	Score 474	DB 11	Length 488
Best Local Similarity	62.2%	Pred. No. 9.3e-40		
Matches 89	Conservative 21	Mismatches 23	Indels 8	Gaps 1
OY	1	MGMNIIFFLVTTAGVHSQVQLVDSGAEVKKRPGSSVKVSKCASGTYTTFDAIOMVROAP	60	
Db	1	MGMNIIFFLVTTAGVHSQVQLVDSGAEVKKRPGSSVKVSKCASGTYTTFDAIOMVROAP	60	
OY	61	GQGLEMGIVINITYNTNTNOKFKGKATMTYDKSTSTAYMELSLRSEPTAYYYCARAA	120	
Db	61	GKSLWMIDINPYNGSTSYNOKFKGKATLTVDKSSSIAYMOLNLTSDSAVYYCARGPV	120	
OY	121	YM-----DYWGQGLTVTVSS 135		
Db	121	YYSFYSYDRGDYWGQGLTVTVSA 143		
RESULT 4				
O91WT3				
ID	PRELIMINARY:	PRT:	481 AA.	
AC	O91WT3:			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	HYPOTHETICAL. 52.0 kDa PROTEIN.			
OS	Mus musculus (Mouse).			
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=COLON;			
RA	Strausberg R.;			
RL	Submitted (SEP-2001) to the EMBL/Genbank/DDAJ databases.			
KW	EMBL; BC013488; AAH13488.1; ..			
DR	Hypothetical protein.			
SK	SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;			
Query Match	64.7%	Score 465.5	DB 11	Length 481
Best Local Similarity	66.2%	Pred. No. 6.7e-39		
Matches 92	Conservative 19	Mismatches 21	Indels 7	Gaps 3
OY	1	MGMNIIFFLVTTAGVHSQVQLVDSGAEVKKRPGSSVKVSKCASGTYTTFDAIOMVROAP	60	
Db	1	MRMSCTIIFLVATATGVSNOVQLDQPGATITVPRGASVKRSKCTSGTTFDYMMNWKQRP	60	
OY	61	GQGLEMGIVINITYNTNTNOKFKGKATMTYDKSTSTAYMELSLRSEPTAYYYCAR---	117	
Db	61	GQGLEMGIVADIDPDSYTNOKFKG-TTLTVPTSSSAAYMLLSITLSEDSAAVYFCARGPR	119	
OY	118	-AAYTMDYWGQGLTVTVSS 135		
Db	120	DSSGY--YWGQGLTVTVSS 136		



SO	SEQUENCE	463 AA;	51007 MW;	EAA674C6BBC30783 CXC64:
	Query Match	63.9%;	Score 460;	DB 11; Length 463;
	Best Local Similarity	62.6%;	Pred. No. 2.3e-38;	
	Matches	87; Conservative	21; Mismatches	27; Indels 4; Gaps 1;
OY	1	MGMWNCIIFFLVTTATGAVHSQVOLVDSGAEEVKKPGSSVKVSKASGYTFTDVAIQWRQAP	60	
	: : : :	: :   :   :   :   :   :		
Dd	1	MEMIIFEFLLSGTGAVHSQVOLQDSGAELAPGASVRLSCASGYTFEGYGVSWVKOPT	60	
OY	61	GQGLEMWIGVINLYNTNPNOKFKRAMPYTKSTAYAMELKSIRSEPTTAIVYYCARAAM	120	
	: :   :   :                             : : : :			
Dd	61	GQGLEMWGEIIPGSONTYYSKEFKRKAITLTTPKSSSTIAAHMLSLSDSNAVYPCARSSY	120	
OY	121	Y---MDYWGGTLVTVSS	135	
	: :   :   :   :   :   :			
Dd	121	YSYDLFAFYWGQGLTVTS	139	

RESULT	9			
099L25				
ID	099L25	PRELIMINARY;	PRT;	473 AA.
AC	099L25;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	SMILAR TO RIKEN CDNA 181006009 GENE.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
NCBI_Taxid=10090;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.			
EMBL:	BC003888; AAH03888.1; -			
HSSP:	P01842; 7FAB.			
DR	InterPro: IPR003599; IG.			
DR	InterPro: IPR003597; IG-cl.			
DR	InterPro: IPR003600; IG-1ike.			
DR	InterPro: IPR003006; IG_MHC.			
DR	InterPro: IPR003596; IG_v.			
DR	Pfam: PF00047; Ig; 4.			
DR	SMART: SM00409; IG; 2.			
DR	SMART: SM00407; IGcl; 3.			
DR	SMART: SM00406; IGV; 1.			
DR	SMART: SM00410; IG_1like; 1.			
DR	PROSITE: PS00290; IG_MHC; UNKNOWN_1.			
SO	SEQUENCE	473 AA;	52449 MW;	BE9889B/986DA155 CRC64;

	Query Match	63.8%	Score 459;	DB 11;	Length 473;
	Best Local Similarity	60.1%;	Pred.	No. 3e-38;	
	Matches	86;	Conservative	20;	Mismatches 29; Indels 8; Gaps 1
Oy	1	MGWNCIIFFLLVTATGAVHSQVQLVDSGAEVKKRGSSVKYSCRASGYTFTDYALIQWRQAP	60		
Dd	1	MEMSVVFLEFLFSVTGVSHSQVQLDQSDELIVPAGASVKSISCVSGYTTFDHTLIHWKQRP	60		
Oy	61	GQGLEMIGVINIYYNTNPNOKERKAFMTYVKRSTANMEKLSLRESDTAIYYCARA-	119		
Dd	61	EGLGLEMIGITIPRDGSTKNEKFGRKAITLDKRSSSTAAYMLNSLTSEPSAVCFCSRGGS	120		
Oy	120	------WYMDYGOGTLTVSS	135		
Dd	121	IYYGYGLYYFDYWGQGTITVSS	143		
RESULT	1C				
Q9BRV0	Q9BRV0	PRELIMINARY;	PRT;	500	AA.
AC	Q9BRV0;				

```

DT      01-JUN-2001 (TREMblrel. 17, Created)
DT      01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT      01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE      HYPOTHEtical 54.2 kDa PROTEIN.
OS      Homo sapiens (Human) .
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606; 1
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=PROSTATE; 1
RA      Strausberg R.; 1
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC005951; AA005951.1; -.
DR      HSSP; P01789; IMCP.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003600; Ig_like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PR00047; Ig_4.
DR      SMART; SM00409; Ig_4.
DR      SMART; SM00407; Igcl; 2.
DR      SMART; SM00406; IgV; 1.
DR      SMART; SM00410; Ig_1like; 1.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW      Hypothetical protein.
SQ      SEQUENCE 500 AA; 5415 MW; 0A9BF43F2A3CC6D9 CRC64;

```

Query Match	63.2%	Score 455	DB 4	Length 500
Best Local Similarity	61.2%	Pred. No. 8.1e-38		
Matches	90	Conservative 13	Matches 32	Indels 12
				Gaps 1
QY	1	MGMNCTIFFLVLTATGAVSHSOVOLVOSGAEEVKKPGSSSVYSCASGATGTETDAIQWROAP	60	
	1			
	1	MDMTSIIIFLVAALATGAOSQVHLVOSGAEEVMSPGASVRSKCTSIATHTYSIIITWRAP	60	
DB	1	MDMTSIIIFLVAALATGAOSQVHLVOSGAEEVMSPGASVRSKCTSIATHTYSIIITWRAP	60	
QY	61	GGGLEMGIVINITYNTNYNOKFKRATMTYDKSTSTAYAMELISLRSEDTAAYVCARA --	118	
	61			
	61	GGGLEMGWISPSNNTFRAPKFGCRVTLTDTSTSTYMEILRSRSDTAAYVCARRVC	120	
DB	61	GGGLEMGWISPSNNTFRAPKFGCRVTLTDTSTSTYMEILRSRSDTAAYVCARRVC	120	
QY	119	-----AMTMDYWGCGILVTYVSS	135	
	119			
DB	121	SYSSCONDYIIYYIMDVWGKGTIVYSS	147	

RESULT	11		
ID	09UL92		
AC	09UL92	PRELIMINARY;	PRT; 124 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	MOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,		
RT	Young D.C.;		
RT	"Mosin-reactive autoantibodies in rheumatic carditis and normal fetus.";		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL; AF035022; AAD56558.1; -		
DR	HSSP; P01772; 2F8A.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_V.		
DR	Pfam: PF00047; Ig; 1.		



[illegible]

RESULT	15		
09UL89			
ID	09UL89	PRELIMINARY:	PRT: 116 AA.
AC	09UL89;		
DT	01-MAY-2000 (Tremblrel, 13, Created)		
DT	01-MAY-2000 (Tremblrel, 13, last sequence update)		
DT	01-DEC-2001 (Tremblrel, 19, last annotation update)		
DE	MOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FEAGMENT).		
OS	Homo sapiens (Human).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Wu X., Liu B., Van der Werpe P.L., Kalls N.N., Berney S.M.,		
RT	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL: AF035025; AAD56261.1; -		
DR	HSSP: P01810; 2FBJ		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_v.		
DR	Pfam: PF00047; Ig_1.		
DR	SMART: SM00406; IGV; 1.		
FT	NON_TER	1	1
FT	NON_TER	116	116
SO	SEQUENCE	116 AA; 12605 MW; C8F9131DE13EA898 CRC64;	

Query Match	60.7%	Score 437	DB 4	Length 116
Best Local Similarity	75.0%	Pred. No. 8.8e-37		
Matches 87	Conservative 7	Mismatches 18	Indels 4	Gaps 1

Qy	24	VOSGAEEVKKPGSSVAVSCASASFTTDAIQWROAPGGGLEMGIGYINITYONTNNOKF	833
Db	1	VOSGAEEVKKPGSSVAVSCASASGTFSSVAISWROAPGGGLEMGIGITPIIDIANVAKOF	600
Qy	84	KGKATMTYDKSTSTAYMELLSLRSEDYATVYCARA-----ATMTDYGCGSTLYTVSS	135
Db	61	QGRVITITADKSTSTAYMELLSLRSEDYATVYCASSWNGYWFETDLRGRTLTAVSS	116

Search completed: August 26, 2002, 15:05:03  
Job time: 367 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2002, 14:57:46 ; Search time 42.03 Seconds

(without alignments)  
356.768 Million cell updates/sec

Title: US-09-249-011-6

Perfect score: 720  
Sequence: 1 MGNMCIIFELVTATRGVHSQ.....AAAMWMDYWGCGTLVTVSS 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:\*

2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:\*

6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:\*

7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:\*

8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:\*

9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:\*

10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:\*

11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*

12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:\*

13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:\*

14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:\*

15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:\*

16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:\*

17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:\*

18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:\*

19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:\*

20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720	100.0	135	21	AA807965
2	627	87.1	135	21	AA807963
3	585.5	81.3	470	21	AAW90935
4	582.5	80.9	470	21	AAW90933
5	581.5	80.8	470	21	AAW90934
6	579.5	80.5	470	19	AAW83037
7	579.5	80.5	470	21	AAW14779
8	579.5	80.5	470	21	AAW90929
9	573.5	79.7	140	15	AAW55556
10	567.5	78.8	470	21	AAW90936
11	566.5	78.7	145	19	AAW83038

12	566.5	78.7	145	21	AAW14775	Fragment of human
13	566.5	78.7	145	21	AAW90925	Humanised anti-Fas
14	566.5	78.7	470	19	AAW83036	Anti-Fas humanised
15	566.5	78.7	470	21	AAW14776	Humanised anti-Fas
16	566.5	78.7	470	21	AAW90926	Humanised HFE7A de
17	554	76.9	588	19	AAW71880	Anti-human Fas hum
18	554	76.9	588	21	AAW12917	Anti-human Fas imm
19	547	76.0	515	22	AAW52162	Humanised HMG-1 F
20	547	76.0	517	22	AAW52154	Humanised HMG-1 F
21	547	76.0	519	22	AAW52164	Humanised HMG-1 F
22	547	76.0	519	22	AAW52165	Humanised HMG-1 F
23	547	76.0	521	22	AAW52163	Humanised HMG-1 F
24	547	76.0	525	22	AAW52166	Humanised HMG-1 F
25	547	76.0	527	22	AAW52155	Humanised HMG-1 F
26	547	76.0	529	22	AAW52168	Humanised HMG-1 F
27	547	76.0	531	22	AAW52167	Humanised HMG-1 F
28	547	76.0	729	22	AAW52158	Humanised HMG-1 h
29	547	76.0	730	22	AAW52157	Humanised HMG-1 h
30	547	76.0	731	22	AAW52156	Humanised HMG-1 h
31	547	76.0	739	22	AAW52161	Humanised HMG-1 h
32	547	76.0	740	22	AAW52160	Humanised HMG-1 h
33	547	76.0	741	22	AAW52159	Humanised HMG-1 h
34	546	75.8	135	13	AAW24107	Humanised anti-Tac
35	545	75.7	135	11	AAW06369	Humanised anti-Tac
36	545	75.7	135	22	AAW69653	Humanised anti-Tac
37	541	75.1	461	22	AAW12236	Humanised anti-Tac
38	541	75.1	462	22	AAW12229	Humanised anti-Tac
39	541	75.1	462	22	AAW12234	Humanised anti-Tac
40	541	75.1	464	22	AAW12232	Humanised anti-Tac
41	541	75.1	465	22	AAW12228	Humanised anti-Tac
42	540	75.0	135	21	AAW80289	Humanised anti-Fas
43	537	74.6	135	21	AAW80288	Humanised anti-Fas
44	532	73.9	588	19	AAW71881	Anti-human Fas hum
45	532	73.9	588	21	AAW12918	Anti-human Fas imm

## ALIGNMENTS

RESULT 1	AAW07965	standard; Protein; 135 AA.
ID	AAW07965	
XX	AAW07965;	
AC	AAW07965;	
XX		
DT	14-NOV-2000	(first entry)
XX		
DE	A heavy chain variable region of humanised 351 antibody.	
XX		
KW	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;	
KW	autoimmune disease; infectious disease; inflammatory disorder;	
KW	systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;	
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;	
KW	multiple sclerosis; transplant rejection; proliferative disease;	
KW	leukemia; lymphoma; anemia; sickle-cell anemia; thalassemia;	
KW	aplastic anaemia; myeloid dysplasia syndrome.	
XX		
OS	Synthetic.	
OS	Mus sp.	
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	Peptide	1..19
FT	Protein	/note="signal peptide"
FT	Protein	20..135
FT	Protein	/note="mature protein"
FT	Region	50..54
FT	Region	/note="complementarity determining region 1"
FT	Region	69..85
FT	Region	/note="complementarity determining region 2"
FT	Region	118..124
FT	Region	/note="complementarity determining region 3"
XX		

PN WO200047625-A2.  
 PD  
 PD 17-AUG-2000.  
 XX  
 XX  
 PF 09-FEB-2000; 2000WO-USO3303.  
 PR  
 PR 12-FEB-1999; 99US-0249011.  
 PR 24-JUN-1999; 99US-0339596.  
 XX  
 XX (GEMY ) GENETICS INST INC.  
 PA  
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 PI  
 DR WPI: 2000-524532/47.  
 DR N-PSDB: AAA39694.  
 XX  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 PR  
 PR  
 PS  
 PS Example 3; Fig 2A; 162pp; English.  
 XX  
 XX The present sequence represents the heavy chain variable region  
 CC of the humanised murine antibody 3D1. The antibody has a binding  
 CC specificity to B7 molecules. The antibody is used to construct humanized  
 CC immunoglobulins, which comprise an antigen binding region of non-human  
 CC origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 XX  
 XX Sequence 135 AA;  
 XX

	Query Match	100.0%	Score 720:	DB 21:	Length 135:
	Best Local Similarity	100.0%	Pred. No. 4.le-55:		
	Matches 135:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
Oy	1 MGNMCIIFELVYTAGVHSQVOLNOSGAEEVKRPGSSSVKSKCASGYTFEDVAIOWWROAP	60			
Dd	1 mgmnciliffvlvtatcgvhsqvqlvsggaevkkrpgsssvkscasgyttfdyalqwrqp	60			
Oy	61 GGGLEWIGIVINITYNTNMNOKKKRAITVDKSTSTAYMEUSSLRESDTAVYYCARAAW	120			
Dd	61 ggglewlgvinlyndtnynqkfkgkatmtvcstetaymeisslrsecdavyycaraaw	120			
Oy	121 YMDYWGGGFLTVVSS 135				
Dd	121 ymdywgggcltlvvss 135				
 RESULT 2 AAB07963 ID AAB07963 standard; Protein; 135 AA. XX AC AAB07963; XX DT XX 14-NOV-2000 (first entry) DE XX Amino acid sequence of heavy chain variable region of 3S1 antibody.					
KW	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;				
KW	autoimmune disease; infectious disease; inflammatory disorder;				
KW	systemic lupus erythematosus; diabetes mellitus; insulinits; asthma;				
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;				

KW	multiple sclerosis; transplant rejection; proliferative disease;
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome.
XX	
OS	Mus sp.
XX	
EH	Key
FT	Peptide
FT	1..19
FT	/note- "signal peptide"
FT	20..135
FT	/note- "nature protein"
FT	50..54
FT	/note- "complementarity determining region 1"
FT	69..85
FT	/note- "complementarity determining region 2"
FT	118..124
FT	/note- "complementarity determining region 3"
XX	
PN	WO200047625-A2.
XX	
PD	17-AUG-2000.
XX	
PF	09-FEB-2000; 2000WO-US03303.
XX	
PR	12-FEB-1999; 99US-0249011.
XX	24-JUN-1999; 99US-0339596.
PA	(GEMV ) GENETICS INST INC.
XX	
PI	Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
XX	Gray GS, Knight A, O'hara D, Rupp B, Veldman GW;
DR	WPI: 2000-524532/47.
DR	N-PSDB: AAA59692.
XX	
PT	Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT	from ATCC PTA-263), or B7-2 (derived from ATCC CRL-1524) molecules,
PT	modulates immune responses and can therefore treat e.g. autoimmune
PT	diseases, infectious diseases -
XX	
XX	Example 1: Fig 1A; 162pp; English.

CC	The present sequence represents the heavy chain variable region of the murine antibody 3D1. The antibody has a binding specificity to B7 molecules. The antibody is used to construct humanized immunoglobulins, which comprise an antigen binding region of non-human origin and a portion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematosus, diabetes mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease, inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient or preventing transplant rejection in a transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (stroke-cell anaemia, thalassemia and aplastic anaemia). Inborn errors of metabolism, congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
SC	
XX	Sequence      135 AA;
QY	
	Query Match                         87.1%;    Score 627;    DB 21;    Length 135;
	Best Local Similarity     84.4%;   Pred. NO. 4,6e-47;
	Matches 114;   Conservative    10;   Mismatches    11;   Indels        0;   Gaps           0;
QY	1 MGNWNCIIFFLVTTATGWSQVOVLVOSGAEVKRPSSVKVSKASGYTFPDVAIQWRAP 60
Dd	1 mgwnciffflvvtatgwsqvqlqgspevlvpgeevkvsksgysgytfdaiaqwkgsh 60
QY	61 GGGLCEMIGAIINLYNTNTNOKFKGATPYTKRSTNAFMELSLSRSEPTAYVCARAAW 120
Dd	61 akslswlgvinylnydnctunqkfkakctucvkssstetaymelarlslalyyccaraw 120
QY	121 YMDYGOGGLTVVSS 135



Db 121 ymdywgqglvtvss 135

## RESULT 3

AAW90935 standard; Protein; 470 AA.

AAW90935;

08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Heu 3 protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; hepatotropic; antinfertility; neuroprotective; antiatherosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP990663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY ) SANKYO CO LTD.

Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

WPI: 2000-258930/23.

N-PSDB; AAA11646.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 180-182; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antinfertility, neuroprotective, antiatherosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (inherent, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic

CC the native ligand, do not induce liver disease, and have reduced risk of CC inducing a human anti-murine antibody response. This sequence represents CC a humanised anti-Fas antibody heavy chain construct designated Heu 3 CC which is described in the method of the invention.

SO Sequence 470 AA;

Query Match 81.3%; Score 585.5; DB 21; Length 470;  
Best Local Similarity 81.4%; Pred. No. 6,7e-43;  
Matches 114; Conservative 6; Mismatches 15; Indels 5; Gaps 1;

Oy 1 MGNACIIFLVTTATGCHSOYQVLOSAGAEVKKPGSSVAVSKASGYRTTDAIQWVRAP 60

Db 1 mgwscilflfvalatgvsqqlvqsgaevrkpgasvkskasgylftysmgwvriqap 60

Oy 61 GGGEMGIVNIYYDNTNMYNOKFKGATMTYDKSSTAYMELSSRSDDTAVYCARAA- 119

Db 61 99glewmgelopsdsytnngkfkqkalcitvdstustaymelslrseddavyycaarnrd 120

Oy 120 ---WYMDYWGQGLTVVSS 135

Db 121 ysmwyfdivwgqglvtvss 140

## RESULT 4

AAW90933 standard; Protein; 470 AA.

AAW90933;

08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Heu 1 protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; hepatotropic; antinfertility; neuroprotective; antiatherosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP990663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY ) SANKYO CO LTD.

Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

WPI: 2000-258930/23.

N-PSDB; AAA11644.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 169-170; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Hen 1  
 CC which is described in the method of the invention.

XX Sequence 470 AA;

Query Match 80.9%; Score 582.5; DB 21; Length 470;  
 Best Local Similarity 80.7%; Pred. No. 1.2e-42;  
 Matches 113; Conservative 7; Mismatches 15; Indels 5; Gaps 1;

QY 1 MGWNCIIFELVTATGHSQVQVQSGAEVKKPGSSVSKVSCASGYFTTDAIOMVROAP 60  
 Db 1 mgsccilliflvatcatgshgqqlvsgaevkkgpasvskvscasgyfttsymwqvwkqap 60  
 QY 61 GQGLEWIGVNIITYDNTMYNOKFKGKATMTVDKSTAYMELSSLRSEDTPVYVCARAA- 119  
 Db 61 gqglewmgeldpsdsytnqgkfkqkattlvdststajmelslrsedtavycarnrd 120  
 QY 120 ----WYMDYMGQGTLYTVSS 135  
 Db 121 ysmnwYfdwvqgltlvss 140

RESULT 5

AAW90934 standard; Protein: 470 AA.

AC AAW90934;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX

DE Humanised anti-Fas designed heavy chain Hen 2 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;  
 KW hepatocytic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.  
 OS  
 XX EP990663-A2.  
 PN  
 XX  
 PD 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.  
 PF  
 XX 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 PR  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 XX Serizawa N, Hayayama H, Nakahara K, Tamaki I, Takahashi T;  
 PI WPI: 2000-256930/23.  
 DR N-PSDB: AAA11645.  
 DR  
 XX

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammation or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 PS Claim 2; Page 174-176; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Hen 2  
 CC which is described in the method of the invention.

XX Sequence 470 AA;

Query Match 80.8%; Score 581.5; DB 21; Length 470;  
 Best Local Similarity 80.7%; Pred. No. 1.5e-42;  
 Matches 113; Conservative 7; Mismatches 15; Indels 5; Gaps 1;

QY 1 MGWNCIIFELVTATGHSQVQVQSGAEVKKPGSSVSKVSCASGYFTTDAIOMVROAP 60  
 Db 1 mgsccilliflvatcatgshgqqlvsgaevkkgpasvskvscasgyfttsymwqvwkqap 60  
 QY 61 GQGLEWIGVNIITYDNTMYNOKFKGKATMTVDKSTAYMELSSLRSEDTPVYVCARAA- 119  
 Db 61 gqglewmgeldpsdsytnqgkfkqkattlvdststajmelslrsedtavycarnrd 120  
 QY 120 ----WYMDYMGQGTLYTVSS 135  
 Db 121 ysmnwYfdwvqgltlvss 140

RESULT 6  
 AAW83037  
 ID AAW83037 standard; Protein: 470 AA.  
 AC AAW83037;  
 XX





```
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= Sig_peptide
FT Region 50..54
FT /label= CDRL
FT Region 69..85
FT /label= CDR2
FT Region 118..129
FT /label= CDR3
XX WC09412215-A.
XX 09-JUN-1994.
XX 30-NOV-1993; 93WO-US11612.
XX 01-DEC-1992; 92US-0983946.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Co MS:
XX WPI: 1994-199974/24.
XX N-PSDB: AAO66702.
XX
XX New humanised antibody specific for l-selectin - with murine CDR
XX and human framework regions, inhibits binding of neutrophils to
XX endothelial cells and useful for treating or preventing
XX inflammation
XX
XX Disclosure; Fig. 3b; 60pp; English.
XX
XX An l-selectin-specific IgG1 or IgG4 humanized antibody has CDRs
XX corresponding to those of mouse Mab DREG-200 and heavy and light
XX chain variable region frameworks of the human acceptor antibody Eu.
XX Nucleotide and aa sequences are provided for the DREG-200 light
XX (AA066699, AAR55553) and heavy (AA066700, AAR55554) chain variable
XX regions and the humanized DREG-200 light (AA066701, AAR55555) and heavy
XX (AA066702, AAR55556) chain variable regions. The humanized antibodies
XX can be produced economically in large quantities by expression in
XX mammalian cell culture or in transgenic animals.
XX
XX Sequence 140 AA:
SQ
Query Match 79.7%; Score 573.5; DB:15; Length 140;
Best Local Similarity 78.6%; Pred. No. 2.1e-42;
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;
QY 1 MGVNCTIFFLVTTATGVHSQVQLVQSGAEVKKPGSSSVKSCAKASGYTFTDYAIGWVRQAP 60
DB 1 MGVSCILFFLVATATGYSQVQLVQSGAEVKKPGSSSVKSCAKASGYTFTSYVMHVIRQAP 60
QY 61 GCGLEMGVINYIDNRYNKKFKGKATMYVDKSTMYMELSLRSRSDTAVTYCARAW 120
DB 61 99GLEWISYIYPRYDGTKEKFGYVLTDESTNTAGMISLSIRSDTAVTYCAREAY 120
QY 121 -----YMDYMGQGTLYWYSS 135
DB 121 gnyvryfdwvqgqtlvtvss 140
RESULT 10
AAW90936
ID AAW90936 standard; Protein; 470 AA.
XX
AC AAW90936;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised HFE7A designed heavy chain HHH type protein.
XX
```

```
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thymic; antineoplastic; anti-Fas;
KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
XX Synthetic.
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
XX
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
XX
XX 30-SEP-1998; 98JP-0276882.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
XX N-PSDB: AAA11655.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems
XX
XX Claim 2; Page 188-189; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
XX ligand system, by binding to Fas on the cell surface, and prevents
XX apoptosis in cells with a normal system, by inhibiting binding between
XX Fas and its ligand. The products of the invention have anti-inflammatory,
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
XX immunomodulatory, dermatological, immunosuppressive, thymic,
XX antineoplastic, nephrotropic, antinfertility, neuroprotective,
XX antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
XX apoptosis by binding to cell surface Fas or inhibit it by competitive
XX inhibition of ligand binding. (I) are used to treat and/or prevent
XX diseases associated with the Fas/Fas ligand system, especially systemic
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
XX versus host disease, Sjogren's syndrome, pernicious or hypoplastic
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively
XX inhibit apoptosis in normal cells but selectively induce it in abnormal
XX cells. They bind to both human and murine Fas, so can be evaluated in
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic
XX the native ligand, do not induce liver disease, and have reduced risk of
XX inducing a human anti-murine antibody response. This sequence represents
XX a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
XX which is described in the method of the invention.
XX
XX Sequence 470 AA:
SQ
Query Match 78.8%; Score 567.5; DB:21; Length 470;
Best Local Similarity 78.6%; Pred. No. 2.4e-41;
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;
QY 1 MGVNCTIFFLVTTATGVHSQVQLVQSGAEVKKPGSSSVKSCAKASGYTFTDYAIGWVRQAP 60
DB 1 MGVSCILFFLVATATGYSQVQLVQSGAEVKKPGSSSVKSCAKASGYTFTSYVMHVIRQAP 60
```



DR N-PSDB; AAA72146.  
PT Preventive or treating agent for the diseases caused by an abnormality  
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
PT anti-Fas antibody  
XX  
PS Example 15; Page 88; 139pp; Japanese.  
XX  
CC The invention relates to compositions for the prevention or treatment  
CC of diseases caused by an abnormality in the Fas/Fas ligand system  
CC containing an anti-Fas antibody as the active component. The anti-Fas  
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
CC or a humanised version of HFE7A containing identical CDRs  
CC (complementarily determining regions) to antibody HFE7A. Via its  
CC interaction with Fas, the antibody of the invention acts as a modulator  
CC of apoptosis. The compositions of the invention may therefore be used in  
CC the treatment or prevention of conditions such as autoimmune diseases,  
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
CC and organ graft rejection. Sequences AAb14775-B14776 and AAb14779  
CC represent the heavy chains (or fragments thereof) of various humanised  
CC HFE7A-derived anti-Fas antibodies.  
XX  
SQ Sequence 145 AA:  
XX  
Query Match 78.7%; Score 566.5; DB 21; Length 145;  
Best Local Similarity 78.6%; Pred. No. 8.6e-42;  
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;  
QY 1 MGNWCIIFLVTTATGYSOVOLVSGAENKPGSSVSKVSKASGYFTDYAIGWRQAP 60  
DB 1 MGNWCIIFLVTTATGYSOVOLVSGAENKPGSSVSKVSKASGYFTDYAIGWRQAP 60  
DB 1 MGNWCIIFLVTTATGYSOVOLVSGAENKPGSSVSKVSKASGYFTDYAIGWRQAP 60  
QY 61 GGGLEWIGVINIYDNTNINOKFKGKATMYDKSTAYMELSLRSEDYAVYYCARAA- 119  
DB 61 GGGLEWIGVINIYDNTNINOKFKGKATMYDKSTAYMELSLRSEDYAVYYCARAA- 119  
QY 120 ----WYNDYWGQGTLLVTVSS 135  
DB 120 ----WYNDYWGQGTLLVTVSS 135  
DB 121 YSNWYFDVWGEGLTVTVSS 140  
RESULT 13  
ID AAW90925 standard; Protein; 145 AA.  
XX  
AC AAW90925;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DE Humanised anti-Fas antibody HFE7A heavy chain protein.  
XX  
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;  
KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antinfertility; neuroprotective; antiatherosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX  
OS Synthetic.  
XX  
PN EP990663-A2.  
XX  
PD 05-APR-2000.  
XX  
PF 29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98JP-0276881.  
PR 30-SEP-1998; 98JP-0276882.  
XX  
PA (SANY ) SANKYO CO LTD.  
XX  
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX  
DR WPI; 2000-256930/23.  
DR N-PSDB; AAA11584.  
XX  
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems  
XX  
PS Example reference 15; Page 126-127; 263pp; English.  
XX  
CC This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thymimetic,  
CC antirheumatic, nephrotropic, antinfertility, neuroprotective,  
CC antiatherosclerotic, cardiant and hepatropic activity. (I) Induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A heavy chain which is used in  
CC the method described in the invention.  
XX  
SQ Sequence 145 AA:  
XX  
Query Match 78.7%; Score 566.5; DB 21; Length 145;  
Best Local Similarity 78.6%; Pred. No. 8.6e-42;  
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;  
QY 1 MGNWCIIFLVTTATGYSOVOLVSGAENKPGSSVSKVSKASGYFTDYAIGWRQAP 60  
DB 1 MGNWCIIFLVTTATGYSOVOLVSGAENKPGSSVSKVSKASGYFTDYAIGWRQAP 60  
DB 1 MGNWCIIFLVTTATGYSOVOLVSGAENKPGSSVSKVSKASGYFTDYAIGWRQAP 60  
QY 61 GGGLEWIGVINIYDNTNINOKFKGKATMYDKSTAYMELSLRSEDYAVYYCARAA- 119  
DB 61 GGGLEWIGVINIYDNTNINOKFKGKATMYDKSTAYMELSLRSEDYAVYYCARAA- 119  
QY 120 ----WYNDYWGQGTLLVTVSS 135  
DB 120 ----WYNDYWGQGTLLVTVSS 135  
DB 121 YSNWYFDVWGEGLTVTVSS 140  
RESULT 14  
ID AAW83036 standard; Protein; 470 AA.  
XX  
AC AAW83036;  
XX  
DT 15-MAR-1999 (first entry)  
XX  
DE Anti-Fas humanised antibody HFE7A heavy chain.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= sig\_peptide  
 FT Protein 20..470  
 FT /label= Mat\_protein  
 FT Region 20..140  
 FT /label= Variable  
 FT Region 141..464  
 FT /label= Constant  
 FT Region 50..54  
 FT /label= CDR\_H1  
 FT /note= "claim 9"  
 FT Region 69..84  
 FT /label= CDR\_H2  
 FT /note= "claim 9"  
 FT Region 118..129  
 FT /label= CDR\_H3  
 FT /note= "claim 9"  
 XX  
 PN AU9859701-A.  
 XX  
 PD 08-OCT-1998.  
 XX  
 PF 30-MAR-1998; 98AU-0059701.  
 XX  
 PR 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 PI Atto S, Hideyuki H, Hiroko Y, Jun O, Kiminisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 XX  
 DR WPI: 1998-543440/47.  
 DR N-PSDB; AAV70079.  
 XX  
 PT New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 XX  
 PS Claim 22; Page 212-213; 292pp; English.  
 XX  
 CC This is the amino acid sequence of the VD type humanised heavy  
 CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli  
 CC pGSL7A62 SANK 73397 harbors plasmid pGSL7A62 carrying a fusion  
 CC fragment of the humanised VD type HFE7A heavy chain and DNA  
 CC encoding human IgG1 constant region (see AAV70079), and is deposited  
 CC as FERM BP-6074 (C1ained). The invention provides methods for  
 CC producing humanised antibodies by culturing host cells. Humanised  
 CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable  
 CC of inducing apoptosis in abnormal cells expressing Fas, and of  
 CC inhibiting Fas-induced apoptosis in normal cells. The humanised  
 CC antibodies are used to evaluate, in animal models, treatments of  
 CC diseases that involve Fas/Fas ligand interactions, and also to  
 CC treat such diseases, including autoimmune disease (e.g. systemic

CC lupus erythematosus, Hashimoto's disease, graft versus host disease,  
 CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,  
 CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,  
 CC autoimmune hemolytic anaemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura and  
 CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
 XX  
 SQ Sequence 470 AA:  
 Query Match 78.7%; Score 566.5; DB 19; Length 470;  
 Best Local Similarity 78.6%; Pred. No. 2.9e-41;  
 Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;  
 QY 1 MGNKIIFFLYTATGVSQVQLVQSGAEVKKPGSSVVSCKASGYPFTDVAIQWRAP 60  
 DB 1 mgwscilflflvatatgvsqvlvsgaeavkpgasvkscaagylttsymmqvwkqap 60  
 QY 61 GQGLEWIGVINIYDNTNYNQKFKATPTVDKSTAYMELSLRSEDYAVYCARAA- 119  
 DB 61 gqrlwmgeidspsdytrnqkfkqkalitvdstastaymelslrsedatvycarrnd 120  
 QY 120 ---WYMDYWGQGLTVTVSS 135  
 DB 121 ysnwvfdvfwgglvtvss 140  
 RESULT 15  
 AAB14776  
 ID AAB14776 standard; Protein; 470 AA.  
 XX  
 AC AAB14776;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.  
 XX  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; humanised; antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;  
 KW hepatitis; AIDS; graft rejection; heavy chain.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 OS  
 PN JP2000169393-A.  
 XX  
 PD 20-JUN-2000.  
 XX  
 PF 30-SEP-1999; 99JP-0278301.  
 PR 30-SEP-1998; 98JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 PI  
 DR WPI: 2000-485645/43.  
 DR N-PSDB; AAA72159.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 XX  
 PS Claim 21; Page 95-96; 139pp; Japanese.  
 XX  
 CC The invention relates to compositions for the prevention or treatment  
 CC of diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs



CC (complementarity determining regions) to antibody HEF7A. Via its  
CC interaction with Fas, the antibody of the invention acts as a modulator  
CC of apoptosis. The compositions of the invention may therefore be used in  
CC the treatment or prevention of conditions such as autoimmune diseases,  
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, AIDS  
CC glomerulonephritis, aplastic anaemia (panmyelopenia), hepatitis, AIDS  
CC and organ graft rejection. Sequences AB14775-B14776 and AB14779  
CC represent the heavy chains (or fragments thereof) of various humanised  
CC HEF7A-derived anti-Fas antibodies

**SQ Sequence 470 AA;**

Query Match	78.7%	Score 566.5;	DB 21;	Length 470;
Best Local Similarity	78.6%	Pred. No. 2.9e-41;		
Matches 110; Conservative	8;	Mismatches 17;	Indels 5;	Gaps 1;

```

Oy      1  MGNANCIIEPLTATNAGVSOVLQVOSAGEYKKEPSSSVKSCAKSGMFTDIAQWROAP  60
Db      1  mgscllflfvalatagvmsqqlvqsgaevkbpasvksvcskasygflfymngvvyqap  60

Oy      61  GGGLEMGIVIVIIYDNNVNNQKFEKGAATPVDSKTSWAMELSLSRESDPAVYVYCAAAA  119
Db      61  ggrlcmgelpsdsyctynqkfkqkatlvtvdsastajmelslsrbedavycarnrd  120

Oy      120  ----WYNDYMGOGTLVPVSS  135
Db      121  ysnmwyfawgqglclvrvss  140

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Search completed: August 26, 2002, 14:58:51  
Job time: 65 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 14:57:46 ; Search time 20.74 Seconds  
(without alignments)  
158,990 Million cell updates/sec

Title: US-09-249-011-6

Perfect score: 720  
Sequence: 1 MGNMCIFFLYTATGCVHSQ.....ARAAMWYMGQGLTVVSS 135

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	573.5	79.7	140	5	PCT-US93-11612-12
3	545	75.7	135	1	US-07-634-278-19
4	545	75.7	135	1	US-08-477-728-19
5	545	75.7	135	1	US-08-477-728-19
6	545	75.7	135	1	US-08-477-728-19
7	545	75.7	135	1	US-08-477-728-19
8	545	75.7	135	2	US-08-303-569B-31
9	531.5	73.8	163	5	PCT-US91-02842-5
10	530.5	73.7	140	3	US-08-836-561-63
11	530	73.6	467	2	US-07-916-098A-45
12	529.5	73.5	136	5	PCT-US93-11611-11
13	529.5	73.5	138	3	US-08-513-968-44
14	529	73.5	139	2	US-08-656-586-8
15	527	73.2	135	1	US-08-137-117D-102
16	527	73.2	135	2	US-08-436-717-102
17	526	73.1	133	4	US-08-718-323A-8
18	525	72.9	139	1	US-08-253-877C-19
19	525	72.9	139	2	US-08-452-164A-19
20	525	72.9	139	3	US-08-603-024-18
21	521	72.4	135	1	US-08-137-117D-100
22	521	72.4	135	2	US-08-436-717-100
23	521	72.4	137	3	US-08-513-968-38
24	518.5	72.0	140	3	US-08-836-561-74
25	515.5	71.6	140	3	US-08-836-561-78
26	515	71.5	135	1	US-08-137-117D-112
27	515	71.5	135	2	US-08-436-717-112

28	511.5	71.0	136	4	US-08-525-539A-63	Sequence 63, Appl
29	508.5	70.6	143	1	US-08-236-520-7	Sequence 7, Appl
30	508.5	70.6	143	5	PCT-US95-05262-7	Sequence 7, Appl
31	507.5	70.5	140	3	US-08-836-561-83	Sequence 83, Appl
32	504.5	70.1	136	4	US-09-450-520A-8	Sequence 8, Appl
33	503.5	69.9	140	1	US-07-946-421-28	Sequence 28, Appl
34	501.5	69.7	123	1	US-08-482-882-53	Sequence 53, Appl
35	501.5	69.7	123	2	US-08-483-389-53	Sequence 53, Appl
36	501.5	69.7	123	2	US-08-487-113D-53	Sequence 53, Appl
37	501.5	69.7	123	2	US-08-473-503-53	Sequence 53, Appl
38	501.5	69.7	123	2	US-08-483-932-53	Sequence 53, Appl
39	501.5	69.7	123	2	US-08-720-420A-53	Sequence 53, Appl
40	501.5	69.7	123	3	US-08-714-017-53	Sequence 53, Appl
41	501.5	69.7	123	3	US-08-475-680-53	Sequence 53, Appl
42	500.5	69.5	142	2	US-08-476-176B-14	Sequence 14, Appl
43	500.5	69.5	142	3	US-08-127-721A-14	Sequence 14, Appl
44	500.5	69.5	142	3	US-08-485-246A-14	Sequence 14, Appl
45	499	69.3	128	4	US-09-199-149-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-08-579-378A-12  
Sequence 12, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: CO, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579, 378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160, 074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983, 946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschultz, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-579-378A-12

Query Match	79.78;	Score 573.5;	DB 4;	Length 140;
Best Local Similarity	78.68;	Pred. No. 3.7e-50;		
Matches 110;	Conservative	8;	Mismatches 17;	Indels 5; Gaps 1;

[illegible]

```

1      RESULT      2
2      PCT-US93-11612-12
3      Sequence 12, Application PC/TUS9311612
4      GENERAL INFORMATION:
5      APPLICANT: Co, Man Sung
6      TITLE OF INVENTION: Humanized Antibodies Reactive with
7      TITLE OF INVENTION: L-Selectin
8      NUMBER OF SEQUENCES: 12
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: Townsend and Townsend Kourile and Crew
11     STREET: One Market Plaza, Stewart Tower, Suite 2000
12     CITY: San Francisco
13     STATE: California
14     COUNTRY: USA
15     ZIP: 94105
16
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: Patent In Release #1.0, Version #1.25
22
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: PCT/US93/11612
25     FILING DATE:
26
27     CLASSIFICATION:
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: US 07/983,946
30     FILING DATE: 01-DEC-1992
31
32     ATTORNEY/AGENT INFORMATION:
33     NAME: Smith, William M.
34     REGISTRATION NUMBER: 30,223
35     REFERENCE/DOCKET NUMBER: 11823-22
36     TELECOMMUNICATION INFORMATION:
37     TELEPHONE: 415-326-2400
38     TELEFAX: 415-326-2422
39
40     INFORMATION FOR SEQ ID NO: 12:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 140 amino acids
43     TYPE: amino acid
44     TOPOLOGY: linear
45
46     MOLECULE TYPE: protein
47
48     PCT-US93-11612-12

```

```

Query Match          79.74:  Score 573.5; DB 5; Length 140:
Best Local Similarity 78.68:  Pred. No. 3.7e-50:
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

QY 1 MGNMCIIFLLVTTATGVASHVOVLVSGAEVKKKPGSSVYVSCASGTYTFDYAIOWRQAP 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MGNMCIIFLLVATATGVASHVOVLVSGAEVKKKPGSSVYVSCASGTYTFDYVMHWRAQP 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GGGLEMGIVINIIYNTNTYNGKFKKATMYTDKSTSTAYMELSSLRSEETAYTYCARAAW 120
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 61 GGGLEMICIYIIPYNDGTITNKKFKGRVITITSDESTNIAHMLSSLRSDPAIVYYCCAREY 120

QY 121 -----YMDYMGGGLTVYSS 135

Db 121 GNYYVYKFDVMGGGLTVYSS 140

```

RESULT 3 1
US-07-634-278-19
Sequence 19 Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLF, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-19

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[illegible]



Db 121 VFDYWGQGLTVSS 135

```
RESULT 6
US-08-487-200-19
: Sequence 19, Application US/08487200
: Patent No. 5693762
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,200
: FILING DATE: 7-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/634,278
: FILING DATE: 19-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/590,274
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/310,252
: FILING DATE: 13-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/290,975
: FILING DATE: 28-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-002610
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 135 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-487-200-19
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Query Match 75.7%; Score 545; DB 1; Length 135;  
Best Local Similarity 77.8%; Pred. No. 2.5e-47;  
Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

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QY 1 MGWNCIIFLVTATGVHSGVQLVQSGAEVKKPGSSSVVSCASGYFTDYAIQWVRQAP 60
Db 1 MGWMIIFLFLSSTAGVHSGVQLVQSGAEVKKPGSSSVVSCASGYFTSTRMHVVRQAP 60
QY 61 GGGLEWIGVINIYDNTNINOKFKGKATMTYDKSTSTAYMELSLRSRSDTAVVYCARAAW 120
Dk 61 GGGLEWIGVINIYDNTNINOKFKGKATMTYDKSTSTAYMELSLRSRSDTAVVYCARAGG 120
QY 121 YMDYWGQGLTVSS 135
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Db 121 VFDYWGQGLTVSS 135

```
RESULT 7
US-08-303-569B-31
: Sequence 31, Application US/08303569B
: Patent No. 5859205
: GENERAL INFORMATION:
: APPLICANT: Adair, John R.
: APPLICANT: Athwal, Diljeet S.
: APPLICANT: Emtage, John S.
: TITLE OF INVENTION: Humanised Antibodies
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205-15
: STREET: One Liberty Place - 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM/PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/303,569B
: FILING DATE: 07-SEP-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Trujillo, Doreen Yanko
: REGISTRATION NUMBER: 35,719
: REFERENCE/DOCKET NUMBER: CARP-0032
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 31:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 135 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-303-569B-31
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Query Match 75.7%; Score 545; DB 2; Length 135;  
Best Local Similarity 77.8%; Pred. No. 2.5e-47;  
Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

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QY 1 MGWNCIIFLVTATGVHSGVQLVQSGAEVKKPGSSSVVSCASGYFTDYAIQWVRQAP 60
Db 1 MGWMIIFLFLSSTAGVHSGVQLVQSGAEVKKPGSSSVVSCASGYFTSTRMHVVRQAP 60
QY 61 GGGLEWIGVINIYDNTNINOKFKGKATMTYDKSTSTAYMELSLRSRSDTAVVYCARAAW 120
Db 61 GGGLEWIGVINIYDNTNINOKFKGKATMTYDKSTSTAYMELSLRSRSDTAVVYCARAGG 120
QY 121 YMDYWGQGLTVSS 135
Db 121 VFDYWGQGLTVSS 135
RESULT 8
US-08-484-537-19
: Sequence 19, Application US/08484537
: Patent No. 6180370
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
```



```

? APPLICATION NUMBER: US/07/916, 098A
? FILING DATE: July 24, 1992
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/US91/08843
? FILING DATE: No. 5871732ember 27, 1991
? CLASSIFICATION: 424
? APPLICATION NUMBER: 07/618,542
? FILING DATE: No. 5871732ember 27, 1990
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: JOHN J. MC DONNELL
? REGISTRATION NUMBER: 26,949
? REFERENCE/DOCKET NUMBER: 92,310-G
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 715-1000
? TELEFAX: (312) 715-1234
? TELEX: 910/221-5317
? INFORMATION FOR SEQ ID NO: 45:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 467 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-07-916-098A-45

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	Query Match	73.6%;	Score 530;	DB 2;	Length 467;	
	Best Local Similarity	72.5%;	Pred. No.	3,5e-45;		
Matches	103; Conservative	11;	Mismatches	20;	IndeIs	8; Gaps
OY	1 MGNMNCITFFLVTATGVASQVQLVDSGAFEVKRPPSSVKYSKSCASGTFPFDYAIAIOWRRAP	60				
Dd	1 MDMTWRVCCLLAVALGAHSAVOVLDSGGAEVRKPGRASVSKSASCAGTFTSYIHWRCAP	60				
OY	61 GGGLGWISVINYYDNTNYNOKFRKRAITYDKSTSTAYAMELSLRSEDTAVYYCAR---	117				
Dd	61 GGGLEMIWIVINPYNGTGTYDEKEFKRKARVTLDPSTINTAMELSLRESDTA VYYCAREKD	120				
OY	118 ----AAWTMDYGGOGLTVVSS	135				
Dd	121 NYATGAWFA-YWGCGTILVVSS	141				
RESULT	12					

RESULT 12  
PCT-US93-11611-11  
Sequence 11 Application PC/TUS9311611  
GENERAL INFORMATION:  
APPLICANT: Man Sung  
APPLICANT: Landolfi, Nicholas F.  
TITLE OF INVENTION: Humanized Antibodies Reactive with CD18  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11611  
FILING DATE: 30-NOV-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,949  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.



```

; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-45
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PRT-US93-11611-11

Query Match          73.5%; Score 529.5; DB 5; Length 136;
Best Local Similarity 75.7%; Pred. No. 8.8e-46;
Matches 103; Conservative 10; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGWNCILFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGTFITDIATIQWROAP 60
   |||:| ||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MGSMWIFLFLSTAGVHSQVQLVQSGAEVKKPGSSVKVSCKASGTFITSLMHMWKQAP 60

QY 61 GGGLEWIGVINIYDNTNINQKFKATMTVDKSTAYMELSLRSEDPAVYYCAAA--R 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GGGLEWIGNINPSTATDYDNQNDKATLTADSTNATMELSLRSEDPAVYYCANGGD 120

QY 120 WYMDYWGQGTLLTVSS 135
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 FLMDYWGQGTLLTVSS 136

RESULT 13
US-08-513-968-44
; Sequence 44, Application US/08513968
; Patent No. 6114143
; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZOMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
```

```

; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-513-968-44

Query Match          73.5%; Score 529.5; DB 3; Length 138;
Best Local Similarity 73.9%; Pred. No. 8.9e-46;
Matches 102; Conservative 13; Mismatches 20; Indels 3; Gaps 1;

QY 1 MGWNCILFLVTTATGVHSQVQLVQSGAEVKKPGSSVKVSCKASGTFITDIATIQWROAP 60
   |||:| ||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MDWTFWVFCLLAAPGASHQVQLVQSGAEVKKPGASVKVSCKASGTFITPIEMKQNP 60

QY 61 GGGLEWIGVINIYDNTNINQKFKATMTVDKSTAYMELSLRSEDPAVYYCA---R 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GGGLEWIGNHPYSDDTNINKEKFKAKLTVDYDSTNATMELSLRSEDPAVYYCAIHYG 120

QY 118 AAWMDYWGQGTLLTVSS 135
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 SAYAMDYWGQGTLLTVSS 138

RESULT 14
US-08-656-586-8
; Sequence 8, Application US/08656586
; Patent No. 5834597
; GENERAL INFORMATION:
; APPLICANT: Tso, J. Yun
; APPLICANT: Anasetti, Michael S.
; APPLICANT: Cole, Claudio
; TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,586
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-007210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-656-586-8

Query Match          73.5%; Score 529; DB 2; Length 139;
Best Local Similarity 74.1%; Pred. No. 1e-45;
Matches 103; Conservative 10; Mismatches 22; Indels 4; Gaps 1;
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OY 1 MGNWCIIFLVTATGVHSGVOLVQSGAEVKKPKSSYKVSCKASGYFTDYA1QWVRQAP 60  
 Db 1 MGNWCIIFLVTATGVHSGVOLVQSGAEVKKPKSASVYKVSCKASGYFTDYA1QWVRQAP 60  
 OY 61 GGGLEWIGVINIYDNTNRYNOKFKGKATMTVDKSTSTAYMELSLRSEDRAVYYCARAAW 120  
 Db 61 GGGLEWIGVINIYDNTNRYNOKFKGKATMTVDKSTSTAYMELSLRSEDRAVYYCARAAW 120  
 OY 121 YMDYWGOGTLVTYSS 135  
 Db 121 YMDYWGOGTLVTYSS 135

RESULT 15  
 US-08-137-117D-102  
 ; Sequence 102, Application US/08137117D  
 ; Patent No. 5795965  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TSUCHIYA, Masayuki  
 ; APPLICANT: SATO, Koh  
 ; APPLICANT: BENDIG, Mary  
 ; APPLICANT: JONES, Steven  
 ; APPLICANT: SALDANHA, Jose  
 ; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
 ; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
 ; NUMBER OF SEQUENCES: 158  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentlin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/137,117D  
 ; FILING DATE: 20-DEC-1993  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/JP92/00544  
 ; FILING DATE: 24-APR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 4-32084  
 ; FILING DATE: 19-FEB-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 3-95476  
 ; FILING DATE: 25-APR-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WEGNER, Harold C.  
 ; REGISTRATION NUMBER: 25,258  
 ; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 102:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 135 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-137-117D-102

OY Query Match 73.2%; Score 527; DB 1; Length 135;  
 Best Local Similarity 75.6%; Pred. No 1.5e-45;  
 Matches 102; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

Db 1 MDTWRYFCLLAVAPGAHSQVOLVQSGAEVKKPKSASVYKVSCKASGYFTDYA1QWVRQAP 60  
 OY 61 GGGLEWIGVINIYDNTNRYNOKFKGKATMTVDKSTSTAYMELSLRSEDRAVYYCARAAW 120  
 Db 61 GGGLEWIGVINIYDNTNRYNOKFKGKATMTVDKSTSTAYMELSLRSEDRAVYYCARAAW 120  
 OY 121 YMDYWGOGTLVTYSS 135  
 Db 121 YMDYWGOGTLVTYSS 135

Search completed: August 26, 2002, 15:00:19  
 Job time: 153 sec





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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 15:37:07 ; Search time 1863.47 Seconds

(without alignments)  
4447.031 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atgattcacagcagccaggt.....ggaccaagtcggaataaaa 396

Scoring table: IDENTITY\_NUC

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_inu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query Match Length DB ID Description  
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1	340	85.9	462	10	MUSICKPALI	M28833 Mus musculu
2	340	85.9	480	6	A13733	A13733 variable re
3	336.2	84.9	406	10	MMU62050	U62050 Mus musculu
4	333.6	84.2	419	10	MMU97570	U97570 Mus musculu
5	332	83.8	940	6	A44968	A44968 Sequence 24
6	332	83.8	940	6	I64459	I64459 Sequence 24
7	301.4	76.1	401	10	MMHA21LEV	X65774 M.musculus
8	298.2	75.3	402	10	MUSICKALA	M68042 Mouse Ig re
9	296	74.7	336	10	AF163745	AF163745 Mus muscu
10	296	74.7	336	10	MDIGKVAR	Z22063 M.domesticu
11	296	74.7	339	10	AB028876	AB028876 Mus muscu
12	295.2	74.5	408	10	S81289	S81289 IGM kappa c
13	295	74.5	339	10	MUSICKV130	L16819 Mus musculu
14	292.8	73.9	336	10	MDIGKVAI	Z22039 M.domesticu
15	292.8	72.9	339	6	MDIGKVAU	A47611 Sequence 3
16	288.6	72.9	399	6	A80111	A80111 Sequence 3
17	288.6	72.3	336	10	MMJ222607	AJ222607 mouse DNA
18	286.4	72.3	337	10	S74056	S74056 Ig VKI-19G2
19	286.4	72.1	439	6	A62621	A62621 Sequence 40
20	285.4	72.1	460	6	A62617	A62617 Sequence 36
21	285.4	71.9	336	10	MMIKACLV	Z31353 M.musculus
22	284.8	71.9	336	10	MUSICKADU	M37022 Mouse Ig re
23	284.8	71.9	336	10	MUSICKADV	M37023 Mouse Ig re
24	284.8	71.9	339	10	MMU60464	U60464 Mus musculu
25	284.8	71.9	339	10	MMU55647	U55647 Mus musculu
26	284.4	71.8	336	10	MMU55674	U55674 Mus musculu
27	284.2	71.8	336	10	MDIGKVAQ	Z22060 M.domesticu
28	283.2	71.5	342	6	AR135863	AR135863 Sequence
29	283.2	71.5	764	10	MMY15982	Y15982 Mus musculu
30	281.8	71.2	339	10	MMU344368	AJ344368 Mus muscu
31	281.6	71.1	600	10	AF349145	AF349145 Mus muscu
32	281.6	71.1	336	10	MMU55673	U55673 Mus musculu
33	281.4	70.9	399	10	MUSFABA	M95574 M.musculus
34	280.6	70.9	399	10	MMIGGVJ5	X02181 M.musculus
35	279.8	70.7	411	10	AR063210	AR063210 Sequence
36	279.8	70.7	1443	6	A94042	A94042 Sequence 23
37	279	70.5	427	6	AX011127	AX011127 Sequence
38	279	70.5	463	6	AR109948	AR109948 Sequence
39	279	70.5	8068	6	A94046	A94046 Sequence 27
40	279	70.5	8068	6	AX011131	AX011131 Sequence
41	279	70.5	336	10	MUSICKADM	M37024 Mouse Ig re
42	278.4	70.3	336	10	MMU55675	U55675 Mus musculu
43	278	70.2	747	6	BD0009690	BD0009690 Anti-P53
44	277.8	70.2	747	12	AC0131533	AJ131533 Synthetic
45	277.8	70.2				

## ALIGNMENTS

RESULT 1  
MUSICKPALI 462 bp mRNA linear ROD 18-NOV-1994  
LOCUS Mus musculus Iqk chain (anti-Pseudomonas aeruginosa lipoprotein I  
DEFINITION Mus musculus Iqk chain (anti-Pseudomonas aeruginosa lipoprotein I  
M28833  
ACCESSION M28833.1 GI:576599  
VERSION V-segment; anti-lipoprotein antibody; immunoglobulin kappa-chain;  
KEYWORDS immunoglobulin light chain.  
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) hybridoma CDNA  
to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 462)  
AUTHORS Margot,M., Eckhardt,A., Ehret,W., von Specht,B.U., Duchene,M. and  
Domdey,H.  
TITLE Cloning and characterization of cDNAs coding for the heavy and  
light chains of a monoclonal antibody specific for Pseudomonas  
aeruginosa outer membrane protein I  
JOURNAL Gene 74 (2), 335-345 (1988)  
MEDLINE 89232725  
COMMENT On Nov 28, 1994 this sequence version replaced gi:342017.

FEATURES  
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/organism="Mus musculus"  
/strain="BALB/c"  
/sub\_species="domesticus"  
/db\_xref="taxon:10090"  
/cell\_line="Mab 6M4"  
/tissue\_type="hybridoma"  
1. .462  
/gene="Igk"  
19. .>462  
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/protein\_id="AA53292.1"  
/db\_xref="GI:576600"  
/translation="MDSQAOVILILLVSGTCGDIVMSQSSSLAVSAGEKVTMSCK  
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SVQADLAVYCKOSYNLRTFGGKLEIKRADAPVTSIFPPSE"

sig\_peptide  
19. .78  
/gene="Igk"  
79. .>462  
/gene="Igk"  
/product="Immunoglobulin kappa chain"

BASE COUNT 114 a 116 c 121 g 111 t

ORIGIN

Query Match 85.9%; Score 340; DB 10; Length 462;  
Best Local Similarity 91.2%; Pred. No. 2.1e-103;  
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 atgattcacagagccaggtctctatattgctgctgctatggtatcgtgacccgtggtg 60  
Db 19 ATGGAATTCACAGGCCAGGCTTCTATATGCTCTGCTGATGAGGTATCTGTGAGTGGG 78  
Qy 61 gacattgctgacacagctccagatccctgctgctgtaagcttagagagagagccact 120  
Db 79 GACATTGTGATGTACACAGTCTCCATCCTCGTGTGTGACACAGAGAGAGAGTCACT 138  
Qy 121 attagctgcaaatccagctcagctcagctcagctcagctcagctcagctcagctc 180  
Db 139 ATGAGCTGCAAAATCCAGTCAAGAGTCTGCTCAACAGTATACCCGAAAGACTTCTTGCT 198  
Qy 181 tggtaacacagagaacacagagcagctcctaaactgctgctcagctcagctcagctcag 240  
Db 199 TGGTACCACAGCAAAACAGGAGGAGTCTCTAACTGCTATCTAGCGCATCCACTAGC 258  
Qy 241 gaactcgggggtccctcagctcagctcagctcagctcagctcagctcagctcagct 300  
Db 259 GAATCTGGGGTCCCTGATGCTTTCACAGGAGTGTGAGATCTGGACAGATTCACCTCACC 318  
Qy 301 atcagcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 360  
Db 319 ATCAGCAGTGTGCAAGCTGCAAGCTGCGAGTTTATTACTGCAAGCAATCTTAAATCTT 378  
Qy 361 tacacgttcggacagaggaaccaagctggaataaaa 396  
Db 379 CGGACGTCGGTGGAGGACCAACGATGGAATCAAA 414

RESULT 2  
LOCUS A13733 480 bp DNA linear PAT 03-JAN-1994  
DEFINITION variable region of a monoclonal antibody which cross reacts with 19 known P.aeruginosa serotypes.  
ACCESSION A13733  
VERSION A13733.1 GI:491741  
KEYWORDS  
SOURCE % synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1. (bases 1 to 480)

AUTHORS Domdey, H., Marget, M. and von Specht, B.U.  
TITLE Monoclonal antibodies to Pseudomonas aeruginosa, their production and use  
JOURNAL Patent: EP 0338395-A 1 25-OCT-1989;  
BEHRINGWERKE Aktiengesellschaft  
FEATURES  
source  
1. .480  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
37. .>480  
/codon\_start=1  
/transl\_table=11  
/product="V region of a monoclonal antibody, cross reacts with 19 P.aeruginosa serotypes"  
/protein\_id="CAA01126.1"  
/db\_xref="GI:491742"  
/translation="MDSQAOVILILLVSGTCGDIVMSQSSSLAVSAGEKVTMSCK  
SSQSLNSTRKNFLAWYQKPGQSKLITWASTRESGVPRFTGSGSDPTLITIS  
SVQADLAVYCKOSYNLRTFGGKLEIKRADAPVTSIFPPSE"

BASE COUNT 115 a 117 c 136 g 112 t

ORIGIN

Query Match 85.9%; Score 340; DB 6; Length 480;  
Best Local Similarity 91.2%; Pred. No. 2.2e-103;  
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 atgattcacagagccaggtctctatattgctgctgctatggtatcgtgacccgtggtg 60  
Db 37 ATGGAATTCACAGGCCAGGCTTCTATATGCTCTGCTGATGAGGTATCTGTGAGTGGG 96  
Qy 61 gacattgctgacacagctccagatccctgctgctgtaagcttagagagagagccact 120  
Db 97 GACATTGTGATGTACACAGTCTCCATCCTCGTGTGTGACACAGAGAGAGAGTCACT 156  
Qy 121 attagctgcaaatccagctcagctcagctcagctcagctcagctcagctcagctc 180  
Db 157 ATGAGCTGCAAAATCCAGTCAAGAGTCTGCTCAACAGTATACCCGAAAGACTTCTTGCT 216  
Qy 181 tggtaacacagagaacacagagcagctcctaaactgctgctcagctcagctcagctcag 240  
Db 217 TGGTACCACAGCAAAACAGGAGGAGTCTCTAACTGCTATCTAGCGCATCCACTAGG 276  
Qy 241 gaactcgggggtccctcagctcagctcagctcagctcagctcagctcagctcagct 300  
Db 277 GAATCTGGGGTCCCTGATGCTTTCACAGGAGTGTGAGATCTGGACAGATTCACCTCACC 336  
Qy 301 atcagcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 360  
Db 337 ATCAGCAGTGTGCAAGCTGCAAGCTGCGAGTTTATTACTGCAAGCAATCTTAAATCTT 396  
Qy 361 tacacgttcggacagaggaaccaagctggaataaaa 396  
Db 397 CGGACGTCGGTGGAGGACCAACGATGGAATCAAA 432

RESULT 3  
LOCUS MMU62050 406 bp mRNA linear ROD 19-FEB-1997  
DEFINITION Mus musculus polyreactive autoantibody, immunoglobulin light chain kappa mRNA, partial cds.  
ACCESSION U62050  
VERSION U62050.1 GI:1438580  
KEYWORDS  
SOURCE house mouse;  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS D'Alva, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P.M. and Dighiero, G.  
TITLE Structural and affinity studies of IgM polyreactive natural autoantibodies

JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1, Immunol. 158 (2), 968-976 (1997)	97146071	2 (bases 1 to 406)	Diaw, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P.M. and Dighiero, G.	Direct Submission	Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris 75724 Paris Cedex 15, France	Location/Qualifiers
source	1. 406	/organism="Mus musculus"	/strain="(CBA/NxBALB/C)F1"	/db_xref="taxon:10090"	/sex="male"	/note="hybridoma M25-9; 6-day-old spleen cells fused with SP2/0 myeloma cells"
CDS	<1..>406	/codon_start=1	/product="polyreactive autoantibody, immunoglobulin light chain kappa"	/protein_id="AAB47613.1"	/db_xref="GI:1439581"	/translation="QVLTLLILMWSGTCGDIVMSQSPSLAVSAGEKYTWCKSSQSTLNSRKNRYLAWYQOKPGQSPKLLIYMTSTESGVPDRFTSGSGTDPTLTIISSVOAALDVAAYCQSNLYVTGFGGTRKLEIKRAADAAFTV"
BASE COUNT	101 a	99 c	108 g	98 t		
ORIGIN						
Query Match	84.9%	Score 336.2;	DB 10;	Length 406;		
Best Local Similarity	92.7%;	Pred. No. 4.1e-102;				
Matches 353; Conservative	0;	Mismatches 28;	Indels 0;	Gaps 0;		
OY	16	cagggtcttatatgtctgtctgtctatgggtatctggtacactgtgggagacatgtgtctgaca	75			
Db	1	CAGGTCTTATATTTCTGTCTATGGGTATCTGGTACCTGGGGACATGTGATGTCA	60			
OY	76	cagttccagatctccctgtgctgtaagcttagagagagagggccacattagctgcgaatcc	135			
Db	61	CAGTCTTCATCTCCCTGTGCTGTGTGCAGCAGAGAGAAAGTACTACTGAGCTGCATATCC	120			
OY	136	agtcagagtcgtctcaacagtagaacccgagagaaactacttggcttgtgtacacagagaa	195			
Db	121	AGTCAGAGTCTCTCAACAGTAGAACCAGAAAGAACTACTTGGCTTGTACACAGCAGAA	180			
OY	196	ccagggcagcctctctaaactgtctatctactgtggcaatcactaggaatctggtgtccct	255			
Db	181	CCAGGCGAGTCTCCCTAAACTGCTGATCTACTGGGCATCCATCAGGGAATCTGGGTCCT	240			
OY	256	gagcttcacagtgagagtgatctggagcaagattcaactctacatcagcagctgtcgag	315			
Db	241	GATGCTTCACACGGCAGTGGATCTGGAGCAGATTCACTCTCAACATCAGCAGTGTGAG	300			
OY	316	gctgaagacgtgcagttatctatctactgtcacgcgaatctataatctttacacgltcgagag	375			
Db	301	GCTGAAGACTGCGCAGTTTATTACTGCAAGCAATCTTAAATCTGTACACGTTCCGAGG	360			
OY	376	gggaccacagtggtgaataaaa	396			
Db	361	GGGACCAAGCTGGAGATAAA	381			
RESULT	4					
LOCUS	MMU97570	419 bp	mRNA	linear	ROD 11-JUN-1997	
DEFINITION	Mus musculus immunoglobulin light chain variable region (Igh)					
ACCESSION	U97570					
VERSION	U97570.1	GI:2183076				
KEYWORDS	house mouse.					
SOURCE	Mus musculus					

REFERENCE	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 419)
TITLE	Feljo,G.C.S., Sabbaga,J., Carneiro,C.R.W. and Brigido,M.M. Variable region structure and staphylococcal protein A binding specificity of a mouse anti-Iaminin receptor monoclonal Igm
JOURNAL	Immunology (1997) In press
REFERENCE	2 (bases 1 to 419)
AUTHORS	Brigido,M.M.
TITLE	Direct Submission
JOURNAL	Submitted (15-APR-1997) Biologia Celular, Universidade de Brasilia, Campus Universitario, Asa Norte, Brasilia, DF 70910-900, Brazil
FEATURES	Location/Qualifiers
source	1..419
gene	/organism="Mus musculus"
CDS	/strain="Balb/c"
	/db_xref="taxon:10090"
	/cell_line="IH2"
	/cell_type="hybridoma"
	1..>419
	/gene="Igk"
	21..>419
	/gene="Igk"
	/note="rearranged Vx8 to Jk1 region"
	/codon_start=1
	/product="immunoglobulin light chain variable region"
	/protein_id="AAB60862.1"
	/db_xref="GI:2183077"
	/translation="MDSQAVLILLLVSTCGDIYMSQSPSSLSAGEKTYMSCK
	SSQSLSTRNRYLAWYQKPGQSPKLLIYWASTRESGVPDRFTGSGSDFTLTIS
	SVQAEELAIYCKOSYLNFLFGGGPKLEIKR"
BASE COUNT	105 a 101 c 115 g 98 t
ORIGIN	
Query Match	84.2%; Score 333.6; DB 10; Length 419;
Best Local Similarity	90.2%; Pred. No. 3.1e-101;
Matches 357; Conservative	0; Mismatches 39; Indels 0; Gaps 0;
OY	1 atgagttcaacagagccaggtcttatattgtcgtcgtcataggtatctggcaactgtgg 60
Db	21 ATGGATTTCACAGGCCAGGTTCTTATTTGGTGTGCTATGGTATCTGTGTAACCTGTGG 80
OY	61 gacattgtactaacagctctccagatccctgcgtgctgaagcttagagagagggcaact 120
Db	81 GACATTGTGATGTCAACAGTCTTCATCTCCTCGCTGTGTACGACGAGAGAGAGGTCACT 140
OY	121 attagctgcaaatccagtcagtcagtcctcaacagtagaaccgagagaaacttctgct 180
Db	141 ATGAGACTGCAATTCACAGTCAGTGTGCTCAAAAATAGAACCCGAGAGAAATTACTTGCT 200
OY	181 tggatccagcagaaaccagggcagcctccctaaactgtcgtactactgggcatccactagg 240
Db	201 TGGTACGACGCAAAACAGGGCAGCTCTCCCAAAACGTGATCTACTGTGGCATCTCCAGT 260
OY	241 gaattgggggtccctgcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
Db	261 GAATGTGGGGTCCCTGATCGCTTCCACAGGCACTGATGTGGACAGATTCTTCACTTCAAC 320
OY	301 atcaagcagctctgcaggtctgaagacgttggcagtttattactgcagcgaactctataactt 360
Db	321 ATCAGCAGATGTCACAGGCTGGAAGACTGGCAATTATTACTGCAAGCAATCTTATATCTT 380
OY	361 taacaagtcgcagacagggagccaaggtgggaataaaa 396
Db	381 CGGACGTTTCGGTGGAGGCCCAAGCTGGAAATCAAA 416
RESULT	5
LOCUS	A44968 940 bp DNA linear PAT 07-MAR-1997
DEFINITION	Sequence 24 from Patent W09151382.
ACCESSION	A44968

VERSION	A44968.1	GI:2299554
KEYWORDS		
SOURCE	unidentified.	
ORGANISM	unidentified.	
REFERENCE	unclassified.	
AUTHORS	1 (bases 1 to 940)	
TITLE	Rose,M.S., Boot,C., Copley,C.G., Paterson,D.S., Hall,S.M., Wright,A.F. and Blakey,D.C.	
JOURNAL	BINDING STRUCTURES DIRECTED AGAINST THE CA55.1 ANTIGEN Patent: WO 9515382-A 24 08-JUN-1995; ZENECA LTD (GB)	
COMMENT	Other publication GB 2297751 960814 Other publication CA 2174512 950608 Other publication ZA 9409266 950605 Other publication AU 113095 950619.	
FEATURES	Location/Qualifiers 1..940	
source	/organism="unidentified" /db_xref="taxon:32644"	
BASE COUNT	241 a 266 c 213 g 220 t	
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Query Match	83.8%;	Score 332;	DB 6;	Length 940;
Best Local Similarity	89.9%;	Pred. NO. 1.1e-100;		
Matches 356;	Conservative	0;	Mismatches 40;	Indels 0;
				Gaps 0;

Oy	1	atgatttcacagagcccaagttctctatattgcgcgcgcataagttatcttcggaccctctg	60
Db	10	ATGGATTTCACAGGCCCAAGTCTTATTATTGGCTGCTGTATGGGATATCGAAGCTGTGGG	69
Oy	61	gacatttgctgcacacagttctccagattccctgcgtctgtaagcttagaagagagggccact	120
Db	70	GACATTGTGATGTACACAGTCTCCATCTCCCTGCGCTGTGTACAGCAGAGAGAGAGGTCAAC	129
Oy	121	attagctgcgaatcccaagtcagaagctctgcctcaacagtagaaccgcgagaaactatctgct	180
Db	130	ATGAGCTGCAAAATCCAGATCAGATCAGATCTCCTCACACATAGAACCCGGAAGAACTACTTGGCT	189
Oy	181	tgtgtccagacgaagaaacagagcgagcgtcttaactgcgtctgatatctactgagcatccaatgg	240
Db	190	TGTGTACCAAGCAAGACCCAGGGCAGTCTCTTAACATGCTCATATATTGGGCATCCACTAGG	249
Oy	241	gaattctgggtccctcgatcgcgtctcagcttcagctggcagctgagatctcgagacgatttcaactccacc	300
Db	250	ACATCTGGGGTCCCGATGATCGCTTCACAGGCATGGATGGGACAGATTTCACTCTCACG	309
Oy	301	atccagcagctctgcagagcttgaagaagctggcagttatctactcaagcaaatctataactct	360
Db	310	ATCACCAGATGTCACAGGCTGTAACACCTCGGCAATTTATTACTGCACAACTATATCTTT	369
Oy	361	tacagcttcgcagcagggagcaacaggttggaataataaa	396
Db	370	CGGAGCTTGCGTGGAGGCCCAAGCTGTGGAAATCAAA	405

RESULT	6
LOCUS	164459
DEFINITION	I64459 Sequence 24 from patent US 566357.
ACCESSION	164459
VERSION	I64459.1 GI:2481353
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 940)
TITLE:	Rose,M.Samuel., Boot,C., Copley,C.Graham., Paterson,D.Stephen., Hall,S.Margaret., Wright,A.Fitman. and Blakey,D.Charles. Antibodies recognizing tumor associated antigen CA 55.1 Patent: US 566357-A 24 09-SEP-1997;
JOURNAL	Location/Qualifiers
FEATURES	1..940
SOURCE	5

BASE COUNT	241 a	266 c	213 g	220 t	
ORIGIN	/organism="unknown"				
Query Match	83.8%; Score 332; DB 6; Length 940;				
Best Local Similarity	89.9%; Pred. No. 1,1e-100;				
Matches 356;	Conservative 0; Mismatches 40; Indels 0; Gaps 0;				
OY	1 atgatacacaagagccaggctctatattcgtctgtctatggatctcgacacctgagg 60				
DB	10 ATGATTCACAGAGCCAGGTTCTTATATGTGCTGTGCTATGGGTATCTGGAACTGTGGG 69				
OY	61 gacattggtctgacacagttctccagatccctgctgtgtaagcttggagagggccact 120				
DB	70 GACATTGTGATGTACACAGTCTTCATCTCCCTGGCTGTCTACAGCAGGAGAGAGGTCTCAC 129				
OY	121 attagctcgaatccagttcagatcgtctgtccaaacagtagaaccggagagaactacttgct 180				
DB	130 ATGAGCTGCAATTCACAGTCTCAGTACAGTCTCCTCAACACTAGAACCCGGAAGAACTACTTGCT 189				
OY	181 tggtaaccagcagaaccagggcagcctctccaaactgtcatctacttgggcatccactagg 240				
DB	190 TGGTACACGACAGACAGACAGGCGACGCTCCTTAACGTGTATCTATTTGGCATCCACTAGG 249				
OY	241 gaactctgggtccctcgatcgtctcactgttgcagtgatgatacttggagacgatttaactctacc 300				
DB	250 ACATCTGGGGTCTCCGTGATCGCTTCACAGGCACTGATCTGGGACAGATTTCACCTCTCAC 309				
OY	301 atccagcagctctcgaagctcgaagagagctggcagtttactctagcagcgaatcttaactct 360				
DB	310 ATCAGCAGTGTCTCAGGCTGTGAAGACTGTGGCAATTTATTACTGCAACCAATCTTATCTCTT 369				
OY	361 tacacgtctcgacagaggagaccagaggttggaataaa 396				
DB	370 CGGACGTTCCGTGGAGGCGCACCAAGTGGAAATCANA 405				
RESULT	7				
LOCUS	MMLA21LEY				
DEFINITION	M.musculus DNA for Ige antibody light chain (VJ).				
ACCESSION	X65774.1				
VERSION	GI:312076				
KEYWORDS	Ige antibody; J-segment; light chain; V-region.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Kofler,H., Schmeegg,I., Geley,S., Heilmberg,A., Varga,J.M. and Kofler,R.				
TITLE	Mechanism of allergic cross-reactions--III. cDNA cloning and variable-region sequence analysis of two Ige antibodies specific for trinitrophenyl				
JOURNAL	Mol. Immunol. 29 (2), 161-166 (1992)				
MEDLINE	92178225				
FEATURES	Location/Qualifiers				
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QY 61 gacattgtctgacacagcttccagattccctgtgtctgtaagcttagagagagggccact 120  
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QY 181 tggtaacagagaacacagagcgacctcctaactgtctgtatctactgtgacactag 240  
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Db 183 TGGTACACAGGGAACACAGGGCAGTCTCTAACTGTGATTTCTGGCATCCACTAGG 242

QY 241 gaattcgggggtccctgtatctgctcagctgagctgagctgagacagattcaactcacc 300  
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Db 243 GAATCTGGGGTCCCTGTATCTCCTTCACAGGAGTGGATCTGGAGCATTTCTACTCTCACC 302

QY 301 atcagcagcttcagagcttgaagctgagctgtattatctacgtcaagcaactctata---at 357  
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Db 303 ATACGACAGTGTGAAGGCTGGAAGCTGGCAGATTATTTACTGTGACATTATATAGCTCT 362

QY 358 ctctacacgttcgagacagggagacaaagtgaataaaa 396  
|||  
Db 363 CCGTACAGCTTCGAGGGGGGACCAACTGGAATAAAA 401

RESULT 8  
MUSIGKALA 402 bp mRNA linear ROD 14-JUL-1993  
LOCUS  
DEFINITION Mouse Ig rearranged K-chain mRNA V-region, 5' end.  
ACCESSION M98042  
VERSION M98042.1 GI:196749  
KEYWORDS V-region; hepatitis; immunoglobulin light chain; processed gene.  
SOURCE Mus musculus (strain BALB/c, sub\_species domesticus) spleen cDNA to mRNA.

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 402)  
Hong, H.-J., Kim, A.-K., Ryu, C.-J., Park, S.-S., Chung, H.-K., Kwon, K.-S.,  
Kim, K.-I., Kim, J., and Han, M.  
Cloning and characterization of cDNA's coding for heavy and light  
chains of a monoclonal antibody specific for pre-S2 antigen of  
hepatitis B virus  
Hepatitis B virus  
Gene 121, 331-335 (1992)  
93077049

JOURNAL MEDLINE  
FEATURES  
source Location/Qualifiers  
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Matches 343; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

BASE COUNT 102 a 102 93 c 100 g 107 t

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Db 123 ATGAGCTGCAAGTCCAGTCAAGGCTTTTATATATAGTAGCAATCAAAAGAACTACTTGGCC 180

QY 181 tggtaacagagaacacagagcgacctcctaactgtctgtatctactgtgacactag 240  
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Db 183 TGGTACACAGGGAACACAGGGCAGTCTCTAACTGTGATTTCTGGCATCCACTAGG 240

QY 241 gaattcgggggtccctgtatctgctcagctgagctgagctgagacagattcaactcacc 300  
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Db 243 GAATCTGGGGTCCCTGTATCTCCTTCACAGGAGTGGATCTGGAGCATTTCTACTCTCACC 300

QY 301 atcagcagcttcagagcttgaagctgagctgtattatctacgtcaagcaactctata---at 357  
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Db 303 ATACGACAGTGTGAAGGCTGGAAGCTGGCAGATTATTTACTGTGACATTATATAGCTAT 360

QY 358 ctctacacgttcgagacagggagacaaagtgaataaaa 396  
|||  
Db 361 CCGTACAGCTTCGAGGGGGGACCTTACTGGAATAAAA 399

RESULT 9  
AF163745 336 bp mRNA linear ROD 20-JUL-2001  
LOCUS  
DEFINITION Mus musculus mab 27.4.1 immunoglobulin light chain variable region  
ACCESSION AF163745  
VERSION AF163745.1 GI:5690296  
KEYWORDS  
SOURCE house mouse.  
MUS musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 336)  
Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.  
Molecular analysis of cross-reactive anti-mysin/anti-streptococcal  
mol. Immunol. 37 (15), 901-913 (2000)  
21179651  
PUBMED 11282394

JOURNAL MEDLINE  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SUBMITTED (03-JUN-1999) Microbiology and Immunology, Oklahoma  
University Health Sciences Center, 940 St. Young Blvd, Oklahoma  
City, OK 73190, USA  
Location/Qualifiers

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BASE COUNT      91 a      83 c      86 g      76 t
ORIGIN

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Best Local Similarity 92.6%; Pred. No. 1,3e-88;
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Db   1  GCACATTGCATGTCACTCAGTCTCCATCCCTCGCTGTGTCAAGCAGAGAGATCTACT 60
Oy   121 attagctgcaaatccagtcagagctgtcttcaacagtagaacccggagaaacttctgct 180
     |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||
Db   61  ATGAGCTGCAAAATTCAGTCAGAGCTGTGGTCAACAGTAGAACCCGAAGAAGTAATGGCT 120
Oy   181 tggtaccagcagaaaaccagggcagcctctctaactgccttgatcttactggcatccactgg 240
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Db   121 TGGTACCAGCAAACAACCAAGGCGAGTCTTAACGTGATCTGAGCATCCACTCACTAAG 180
Oy   241 gaattcggggtccccgaatcagcctttagtgcaagtggatcttgagagagattcaactcaac 300
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Db   181 GAATCTGGGGTGCCCTGCATGTCGCTTCAACAGGACATGATCTGGGACAGATTTCACTCAC 240
Oy   301 atcaagcagctctcagagcttgaagacgttgscagtttatcttcgacgcaactctataactt 360
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Db   241 ATCACCACTGTGTCAGGCTGAAGACCTGGCAGATTATTAATCGAACCAATCTTATATCTG 300
Oy   361 tacacgttcgcagcagggagccaaggttggaataaaaa 396
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Db   301 TACACGTTGCGAGGGGGGACCAAGCTGGAAAAAAA 336

RESULT 10
MDICKVAR
LOCUS       MDICKVAR                      336 bp      mRNA           linear      ROD 05-NOV-1994
DEFINITION M.domesticus Igk variable region.
ACCESSION   Z22063
VERSION     2.22063.1 GI:297629
KEYWORDS    anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.
SOURCE      Mus musculus domesticus
ORGANISM    Mus musculus domesticus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
TITLE       1 (bases 1 to 336)
           Both Igm and Igk anti-DNA antibodies are the products of clonally
           selective B cell stimulation in (NZB x NZW)F1 mice
JOURNAL     J. Exp. Med. 176 (3), 761-779 (1992)
MEDLINE     92381444
REFERENCE   2 (bases 1 to 336)
AUTHORS     Marion,T.N.
TITLE       Direct Submission
JOURNAL     Submitted (23-MAR-1993) Tony N. Marion, Microbiology and
           Immunology, University of Tennessee, Memphis, 858 Madison Avenue,
           Memphis, TN, 38163, USA
FEATURES
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DB	61	ATGAGCTGCAAAATCCAGTCAGACAGTGTGCTCAACAGTAAACCCGAAAGAACTACTTGCT	120				
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DB	121	TGGTACCAAGCAAAACCGAGGCGACAGTCTCTTAACGTGATCTACTGGGCATCCACTAGG	180				
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DB	181	GAATGTGGGGTCCCTGATGCGCTTCAACAGCGAGTGTGGGACAGATTTACTCTCACCC	240				
QY	301	atccagcagctctcgaagtcgaagacgttgacgtttacttactcagcagcaactctataactt	360				
DB	241	ATCAGCAGTGTGTCAGAGCTGAAAGACCTGGCAGTTTATCTGCAAGCAATCTTATAATCTG	300				
QY	361	tacacgttcggaagagggagccaaaggttggaataaaaa	396				
DB	301	TACACGTTTCGGAGGGGAGCCACAGCTGGAATAAAAA	336				
RESULT	11						
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DEFINITION	Mus musculus mRNA for 5.2 IgG light chain (variable region),						
ACCESSION	AB028876						
VERSION	AB028876.1						
KEYWORDS	5.2 IgG light chain variable region.						
SOURCE	Mus musculus cell_line:hybridoma 5.2 cDNA to mRNA.						
ORGANISM	Mus musculus						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
TITLE	Yoshida,S., Matsuoka,H., Luo,E., Iwai,K., Arai,M., Sinden,R.E. and						
	Ishii,A.						
	A single-chain antibody fragment specific for the Plasmodium						
	berghel ookinete protein Pbs21 confers transmission blockade in the						
	mosquito midgut						

JOURNAL  
MEDLINE  
20058748  
REFERENCE  
2 (bases 1 to 339)  
AUTHORS  
Yoshida,S.  
TITLE  
Direct Submision  
JOURNAL  
Submitted (11-JUN-1999) Shigeto Yoshida, Jichi Medical School,  
Department of Medical Zoology, Yakushiji 3311-1,  
Minamikawachimachi, Tochigi 329-0498, Japan  
(E-mail:shigeto@jichi.ac.jp, Tel:81-285-58-7339,  
Fax:81-285-44-6489)  
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BASE COUNT 92 a 84 c 87 g 76 t  
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Query Match 74.7%; Score 296; DB 10; Length 339;  
Best Local Similarity 92.6%; Pred. No. 1.5e-88;  
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QY 361 tacacgttcgagcagaggaaccaaggtggaataaaa 396  
DB 301 TACACGTTTCGAGGGGGGAGCAACGCTGGAATAAAAA 336  
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DEFINITION 19M kappa chain variable region (CDR1 to CDR3 region) [rats, LEW,  
S81289  
ACCESSION S81289  
VERSION S81289.1 GI:1326409  
KEYWORDS  
SOURCE Rattus sp. LEW HAR-1 hybridoma cells.  
ORGANISM Rattus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.  
1 (bases 1 to 408)  
AUTHORS  
Borie,D.C., Cramer,D.V., Shirwan,H., Wu,G.D., Rodriguez,O.,  
Chapman,F.A. and Makowka,L.  
TITLE  
Genetic control of the humoral immune response to xenografts. II.  
Monoclonal antibodies that cause rejection of heart xenografts are  
encoded by germ-line immunoglobulin genes  
JOURNAL  
Transplantation 60 (12), 1504-1510 (1995)  
MEDLINE  
96125839  
REMARK  
Genbank staff at the National Library of Medicine created this  
entry (NCBI g1bbsg 176405) from the original journal article.  
This sequence comes from Fig. 4.  
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Query Match 74.5%; Score 295.2; DB 10; Length 408;  
Best Local Similarity 84.1%; Pred. No. 2.8e-88;  
Matches 333; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
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DB 307 ATCAGCAGTGTGTCAGAGCGTGAACACTGCGCTGTTTATTACTGCGACGATCTTAACCTTG 366  
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DB 367 TACACGTTTCGAGGCTGGAACAACTGGAAGTAAA 402  
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LOCUS MUSIGKV130 339 bp mRNA linear ROD 29-OCT-1994  
DEFINITION Mus musculus Ig rearrange kappa-chain gene V19-J1 region.  
ACCESSION L16619

VERSION L16819.1 GI:293622  
KEYWORDS V-region: complementarity determining region; immunoglobulin light chain; kappa-immunoglobulin; processed gene.  
SOURCE Mus musculus (strain NZB/W F1) mRNA.  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 339)  
AUTHORS Lustgarten,D.L., Kavalier,J., Gerhard,W. and Schaff,M.D.  
TITLE The response to a foreign antigen in the autoimmune NZB/W F1 murine strain  
JOURNAL unpublished (1993)  
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Matches 310; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

ACCESSION 222039  
VERSION 222039.1 GI:297576  
KEYWORDS anti-DNA antibody; Igg gene; Igg variable region; immunoglobulin.  
SOURCE western European house mouse.  
ORGANISM Mus musculus domesticus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 336)  
AUTHORS Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.  
TITLE Both Igm and Igg anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZM)F1 mice  
JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)  
MEDLINE 92381444  
REFERENCE 2 (bases 1 to 336)  
AUTHORS Marion,T.N.  
TITLE Direct Submission  
JOURNAL Submitted (23-MAR-1993) Tony N. Marion, Microbiology and Immunology, University of Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA  
FEATURES Location/Qualifiers  
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Db 241 ATCAGCAGTGTGCGAGGCTGAAGACCTGGCAGTTATTACTGCAGCAATCTATATCTG 300

QY 361 tacacgttcgacagggagaccaggtggaataaa 396  
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Db 301 TACACGTTTCGGGGGGGGACCAAGCTGGAATATAAA 336

RESULT 15

MDICKVAVU 336 bp mRNA linear ROD 05-NOV-1994

LOCUS M.domesticus Igh variable region. 222070

DEFINITION 222070.1 GI:297635

ACCESSION anti-DNA antibody; Igh gene; Igh variable region; immunoglobulin.

VERSION western European house mouse.

KEYWORDS Mus musculus domesticus

SOURCE Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ORGANISM 1 (bases 1 to 336)

REFERENCE Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.

AUTHORS Both Igh and Igg anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice

JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)

MEDLINE 92381444

REFERENCE 2 (bases 1 to 336)

AUTHORS Marion,T.N.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-1993) Tony N. Marion, Microbiology and Immunology, University of Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA

FEATURES

source location/Qualifiers

1..336

/organism="Mus musculus domesticus"

/strain="(NZB x NZW)F1"

/isolate="mouse #165"

/db\_xref="taxon:10092"

/chromosome="6"

/sex="Female"

/cell\_line="165.5"

/cell\_type="hybridoma"

/tissue\_type="spleen"

/dev\_stage="somatic variant"

1..336

/gene="Igh"

<1..>336

/gene="Igh"

/function="kappa light chain variable region for anti-DNA antibody; VK8 family"

/codon\_start=1

/product="immunoglobulin variable region"

/protein\_id="CA8004.1"

/db\_xref="GI:297635"

/translation="DIVMSQSPSLAVSAGEKVTMSCKSMOSLLNSTRKRYLAWYQO  
KRGOSPKLIYMASTRSGVDPFRFGSGSGTDETLTISVQAEDLAVYCKOSYNLYT  
FGGSTRKLEIK"

CDS

gene

BASE COUNT 91 a 83 c 86 g 76 t

ORIGIN

Query Match 73.9%; Score 292.8; DB 10; Length 336;  
Best Local Similarity 92.0%; Pred. No 1.8e-87;  
Matches 309; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 61 gacatgtcctgacacagctccagattccctgctgtgaagcttagagagagagccact 120  
|||||  
Db 1 GACATGTGATGTCACAGCTCCATCCCTCGCTGTGCACAGAGAGAGAGTCACT 60

QY 121 attagctgaatcccgtagagctgctcaacagtagaaccgcgagagaactacttgct 180  
|||||  
Db 61 ATGAGCTGCAAACTGACAGAGTGTCTCAACAGTAGAACCCGAAAGAACTACTTGCT 120

QY 181 tggtaaccagagaacacagagcctcctaactgtgattcactgagcactcactagg 240  
|||||

Db 121 TGGTACCAGCAGAAACCAAGGCGACTCTCTTAACCTGATCTACTGGGCATCCACTAGG 180

QY 241 gaatctgggtcccttgatcgcttcagtggcagtgatctggagacatctcactcacc 300  
|||||  
Db 181 GAATCTGGGTCCTTGATCGCTTCACAGGCAGTGATCTGGGACAGATTTCACCTCCACC 240

QY 301 atcagcagctcgcagagctggaagacgttgcaattattactgcagcgaatcttaacct 360  
|||||  
Db 241 ATCAGCAGTGTGACAGGCTGAAGACCTGGCAGTTATTACTGCAAGCAATCTATATCTG 300

QY 361 tacacgttcgacagggagaccaggtggaataaa 396  
|||||  
Db 301 TACACGTTTCGGAGGGGGGACCAAGCTGGAATATAAA 336

Search completed: August 26, 2002, 15:37:10  
Job time: 2209 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 16:13:39 ; Search time 2170.14 Seconds

(without alignments)  
2462.880 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atgattccacagcccaagtc.....ggaccaagtggaataaaa 396

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthu:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estop:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gD\_estcl:\*  
10: gD\_estl2:\*  
11: gD\_htc:\*  
12: gD\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312	78.8	905	10	BF580037 602095235
2	288.6	72.9	864	10	BF111610 602895973
3	272.8	68.9	691	10	BF128999 601811318
4	269.4	68.0	850	10	BG966217 602830117
5	267	67.4	575	10	B1249452 602995789
6	259.4	65.5	964	10	BG757678 602711268
7	258.6	65.3	300	10	BG148633 602571268
8	256.6	64.8	798	10	BG426036 602492715
9	256	64.6	641	9	AM405821 602492715
10	253.4	64.0	643	9	AM390292 602492715
11	251	63.4	886	10	BF674779 602137932
12	249.2	62.9	633	10	BG542772 602571354
13	247.6	62.5	508	9	AM406572 602571354
14	247.6	62.5	819	10	BG686522 602637474
15	247.6	62.5	842	10	BG757770 602714482
16	247.6	62.5	887	10	BF663188 602144432
17	247	62.4	625	10	BF1820438 603034746

18	247	62.4	876	10	BG397563
19	245.6	62.0	921	10	BG569993
20	245.4	62.0	710	10	BG537677
21	244	61.6	388	9	AM951579
22	242.6	61.3	757	10	BG484518
23	242.6	61.3	767	10	BG541967
24	242.6	61.3	1057	10	BG399525
25	242.6	61.2	769	10	BG34966
26	242.2	61.2	761	10	BG536372
27	241.4	61.0	935	10	BG398034
28	241.2	60.9	698	10	BF160019
29	240.6	60.8	573	10	BF128829
30	240	60.6	745	10	BG484741
31	235.8	59.5	541	10	BG547312
32	234.4	59.2	869	10	BG429604
33	234.2	59.1	559	10	BG548150
34	233.6	59.0	878	10	B1837524
35	231.6	58.5	957	10	BG756233
36	231.4	58.4	862	10	BG485664
37	231.4	58.4	867	10	BF128587
38	229.6	58.0	401	9	AV685285
39	229.2	57.9	790	10	BG548131
40	228.4	57.7	533	9	AM802126
41	228.4	57.7	558	10	BF964753
42	227.2	57.4	503	10	BF830413
43	226.6	57.2	550	9	AM404610
44	226.2	57.1	403	9	AV734428
45	225.4	56.9	716	10	BG570035

## ALIGNMENTS

RESULT 1  
BF580037  
LOCUS 602095235F1 NCT\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4209417 5',  
DEFINITION mRNA sequence.  
ACCESSION BF580037  
VERSION BF580037.1 GI:11653749  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
1 (bases 1 to 905)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9775 row: f column: 10  
High quality sequence stop: 757.  
Location/Qualifiers  
1. 905  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4209417"  
/clone\_lib="NCT\_CGAP\_Co24"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: PCMV-SPORE6; Site:1; NotI;  
Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCT\_CGAP Library."

BASE COUNT

248 a 236 c 217 g 204 t

## ORIGIN

Query Match 78.8%; Score 312; DB 10; Length 905;

Best Local Similarity 91.7%; Pred. No. 2e-85; Matches 363; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

QY 1 atgagtcacagagccaggcttctatattgctctgtctatggtatctgacacctgtg 60  
|||||  
DB 18 ATGAGATTTCACAGGCCACAGGTTCTTATTA-TGCTCTGCTATAGGTAATCTGCTGTGGG 76  
QY 61 gacattgtctgacacagctctcagattcccttgctgttaagcttaagagagagccact 120  
|||||  
DB 77 GACA-TGTGATGTACACAGTCTCCATCCCTCCGCTGTGTGTCACAGAGAGAGAGGTCACCT 135  
QY 121 attaagctgaacatccacagtcagagtcgtctcaacagtagaaccggagagaactcttgct 180  
|||||  
DB 136 ATGAACTGCMAATCCAGTCCAGAGTCTGCTCAGACGTAGAACCCGAAAGAACTACTTGGCT 195  
QY 181 tggtagcagagagaacacagagcagcctcctaactgtctgtactctgagagtcacactag 240  
|||||  
DB 196 TGGTACCAGCAGAAACCA-GGCAGTCTCTCTAACTGCTGATCTAGTGGCATCCACTAGC 254  
QY 241 gaactctggggtccctgctatcgtctcaagtcagtcagtcagtcagtcagtcagtcagtc 300  
|||||  
DB 255 GAATCTGGGGTCCCTGATGCTTACAGAGCAGTGTGAGATCTGGACAGATTTCACCTCACC 314  
QY 301 atcagcagctcgtcagcgtcgaagacgtgagcagtcattatctacgcacgcacatcttaact 360  
|||||  
DB 315 ATCAGAGTGTGAGCTGAGACCTGGCAGTTTATTACTGCAAGCAATCTTAAATCTT 374  
QY 361 tacacgtctcgacagagggacacagtcagtcagtcagtcagtcagtcagtcagtcagtc 396  
|||||  
DB 375 TTCACGTCGGCTCGGGGACCAAGTTGGAATATAA 410

## RESULT 2

BI111610 864 bp mRNA linear EST 26-JUN-2001  
LOCUS 602895973f1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:5025715 5',  
DEFINITION mRNA sequence.

ACCESSION BI111610  
VERSION BI111610.1 GI:14562511  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 864)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Lotmar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM1073 row: b column: 20  
High quality sequence stop: 644.  
Location/Qualifiers  
1..864

## FEATURES

source  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone\_image="5025715"  
/clone\_lib="NCI\_CGAP\_Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"

BASE COUNT 230 a 233 c 196 g 205 t

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lotmar Hennighausen/Robin Humphreys,  
NIH"

Query Match 72.9%; Score 288.6; DB 10; Length 864;  
Best Local Similarity 84.5%; Pred. No. 3.2e-78;  
Matches 337; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 atgagtcacagagccaggcttctatattgctctgtctatggtatctgacacctgtg 60  
|||||  
DB 2 ATGAGATTTCACAGGCCACAGGTTCTTATTA-TGCTCTGCTATAGGTAATCTGCTGTGGG 61  
QY 61 gacattgtctgacacagctctcagattcccttgctgttaagcttaagagagagccact 120  
|||||  
DB 62 GACATTGTATGTACACAGTCTCCATCCCTCCGCTGTGTGTCAGATGTGAGAGAGAAATTA 121  
QY 121 attaagctgaacatccacagtcagagtcgtctcaacagtagaaccggagagaactacttgct 180  
|||||  
DB 122 ATGAGCTGCMAATCCAGTCCAGAGTCTGCTCAGACGTAGAACCCGAAAGAACTACTTGGCT 181  
QY 181 tggtagcagagagaacacagagcagcctcctaactgtctgtactctgagagtcacactag 240  
|||||  
DB 182 TGGTACCAGCAGAAACCA-GGCAGTCTCTCTAACTGCTGATCTAGTGGCATCCACTAGC 241  
QY 241 gaactctggggtccctgctatcgtctcaagtcagtcagtcagtcagtcagtcagtcagtc 300  
|||||  
DB 242 GAATCTGGGGTCCCTGATGCTTACAGAGCAGTGTGAGATCTGGACAGATTTCACCTCACC 301  
QY 301 atcagcagctcgtcagcgtcgaagacgtgagcagtcattatctacgcacgcacatcttaact 357  
|||||  
DB 302 ATCAGAGTGTGAGCTGAGACCTGGCAGTTTATTACTGTCAGCAATATTATTAATCTT 361  
QY 358 cttaacagctctcgacagagggacacagtcagtcagtcagtcagtcagtcagtcagtcagtc 396  
|||||  
DB 362 CCCTGGACGTTCCGTTGAGGACCAAGCTGGAATATAA 400

## RESULT 3

BF128999 691 bp mRNA linear EST 24-OCT-2000  
LOCUS 601811318f1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4054205 5',  
DEFINITION mRNA sequence.

ACCESSION BF128999  
VERSION BF128999.1 GI:10968039  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 691)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM894 row: c column: 06  
High quality sequence stop: 682.  
Location/Qualifiers  
1..691

## FEATURES

source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"





CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1M11374 row: b column: 24  
High quality sequence stop: 575.

## FEATURES

source

1..575  
Location/Qualifiers  
/organism="Mus musculus"  
/strain="C57/B6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5151287"  
/clone\_1lb="NCI CGAP Mam5"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lothar Hennighausen/Robin Humphreys,  
NIH"

BASE COUNT 149 a 137 c 139 g 150 t  
ORIGIN

## Query Match

Best Local Similarity 82.7%; Score 267; DB 10; Length 575;  
Matches 330; Conservative 0; Mismatches 65; Indels 4; Gaps 2;

Oy 1 atggaattcacaagccaggtcttataatgtctgtctatggtatggtacatggtggc 60  
Db 9 atggaattcacaagccaggtcttataatgtctgtctatggtatggtacatggtggc 68  
Oy 61 gacattgtctcaacagtcagatccctggtggtgaagcttagaagagggccact 120  
Db 69 gacattgtctcaacagtcagatccctggtggtgaagcttagaagagggcttagc 128  
Oy 121 attagctgcaaaatccagtcagatctgtctcaacagtagaaccgagaaactactggtc 180  
Db 129 atgagctgcacagtcagtcagagcctttttatattagttacatcaaaagaactattttggcc 188  
Oy 181 tggtagcagcagaagaacagagcagcctccttaactgtctatctactgtggtacactagg 240  
Db 189 tggtagcagcagaagaacagagcagcctccttaactgtctatctactgtggtacactagg 247  
Oy 241 gaatctgggtccctgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
Db 248 gaatctgggtccctgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 307  
Oy 301 atcagcagtcctgcaagctggaagcgtgagcagttattactgacagcaatctata--at 357  
Db 308 atcagcagtcctgcaagcgtggaagcgtgagcagttattactgacagcaatctata--at 367  
Oy 358 cttaacagcttcggaacaggggacaaaggtggaataaaa 396  
Db 368 cccgtcacgttcggtgctggagcacaagtcgacactgaga 406

RESULT 6  
LOCUS BG757678 964 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602711268P1 NIH\_MGC\_48 Homo sapiens CDNA clone IMAGE:4851521 5',  
mRNA sequence.  
ACCESSION BG757678  
VERSION BG757678.1 GI:14068331  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 964)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT Robert Strausberg, Ph.D.  
COMMENT Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1CMI694 row: h column: 18  
High quality sequence stop: 784.

## FEATURES

source

1..964  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4851521"  
/clone\_1lb="NIH\_MGC\_48"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pORF7; Site\_1: XhoI;  
Site\_2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 236 a 280 c 238 g 210 t  
ORIGIN

## Query Match

Best Local Similarity 80.1%; Score 259.4; DB 10; Length 964;  
Matches 318; Conservative 0; Mismatches 76; Indels 3; Gaps 1;

Oy 3 ggaattcacagggccaggtcttataatgtctgtctatggtatggtacatggtggc 62  
Db 1 ggaattcacagggccaggtcttataatgtctgtctatggtatggtacatggtggc 60  
Oy 63 catctgtctgacacagtcctcagatccctggtggtgaagcttagagagagggccact 122  
Db 61 catctgtctgacacagtcctcagatccctggtggtgaagcttagagagagggccact 120  
Oy 123 taagctgaatccagtcagagtcgtctcaacagtagaaccgagaaactactgtgctg 182  
Db 121 caactgcmaagtcacagcagaggtttttatracactccacaaatmaaacactactgcttg 180  
Oy 183 gtaaccagagaacccaagggagcctcctaactgtctgactactggtgacatcaggga 242  
Db 181 gtaaccagagaacccaagggagcctcctaactgtctgactactggtgacatcaggga 240  
Oy 243 atctgggtgtccctgacatcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 302  
Db 241 atctgggtgtccctgacatcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
Oy 303 cagcagcttcgcaagctggaagcgtgagcagttattactgacagcaatctata--taact 359  
Db 301 cagcagcttcgcaagcgtggaagcgtgagcagttattactgacagcaatctata--taact 360  
Oy 360 ttacacgttcggaacaggggacaaaggtggaataaaa 396  
Db 361 aaagacgttcggccagagggacaaaggtggaataaaa 397

RESULT 7  
LOCUS BG148633 300 bp mRNA linear EST 01-FEB-2001  
DEFINITION u085b09.v1 Soares\_mouse\_NMGb\_bcell\_mus\_musculus CDNA clone  
IMAGE:3383368 5' similar to SW:KVC\_HUMAN P06314 IG KAPPA CHAIN  
V-IV REGION IBI7 PRECURSOR. ; mRNA sequence.

ACCESSION	BG148633	GI:12652055
VERSION	EST.	
KEYWORDS	house mouse.	
SOURCE	Mus musculus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	NCI-CCAG http://www.ncbi.nlm.nih.gov/ncicagp.	
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
TITLE	Unpublished (1997)	
JOURNAL	Contact: Robert Strausberg, Ph.D.	
COMMENT	Email: cgapbs-re@mail.nih.gov This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:1088364	
FEATURES	Seq primer: -40RP from Gldco.	
SOURCE	Location/Qualifiers 1..300 /organism="Mus musculus" /db_xref="taxon:10090" /clone_image="3383368" /clone_id="Soares_mouse_NMGB_bcell1" /lab_host="DH10B (phage-resistant)" /note="Organ: germinal B-cell; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - o.ligo(dT) primer [5]. TVTACCACATCTGAAGTGGGGAGCGGCCCGCTTTTGTTTTTTTTTTTTTTTTTTTT T 3.); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized; constructed by Bento Soares and A.Patima Bonaldi."	
BASE COUNT	85 a 72 c 79 g 64 t	
ORIGIN		
Query Match	65.3%; Score 258.6; DB 10; Length 300;	
Best Local Similarity	94.9%; Pred. No. 3.9e-69;	
Matches	278; Conservative 0; Mismatches 14; Indels 1; Gaps 1;	
OY	105 aggagagaggcacaattagtctgcaaatccagtcagaagctgtctcaacagttagaccgcg 164 	
DB	5 AGGAGAGAGGTCCTACTAGACCTGCCAATCCAGTCAGAGCTGCTCACAAGAAACCG 64 	
OY	165 aggaagactacttgctgtgtgccagcaaaaacacggcgagcgtcctaactcgtgatcta 224 	
DB	65 AAAGAAGTAAGTCTGGCTTGTCACCAAGAACAAACAGGGCAGTCTCTTAACCTGTATCTA 124 	
OY	225 ctgggcatcacctagggagatctggggctccctgatcgcttccagttgagcagtcggagac 284 	
DB	125 CTGGCATCACCTAGGGAATCTGGGGTCCCGATGCGTTCAACAGCAATGGATCTGGGAC 184 	
OY	285 aga-tttactctcaacctcagcagctctgcagagctgaaagcgtggcagtttaattactgca 343 	
DB	185 AGATTTCACCTCACCATCAGCAAGTGGCAGAGGCTGGAAGACCTGGCACTTTATTAATCTCCA 244 	
OY	344 ccgaactctaatcattcaacagtttcgagacagggagcaaggttgaaaataaa 396 	
DB	245 AGCAATCTTATAATCTGTACACGTTCCGAGGGGGGACCAACTGTGAAATATAAA 297 	
RESULT	8	
LOCUS	BG426036	
DEFINITION	602492717f1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:460658 5', mRNA sequence.	
ACCESSION	BG426036	
VERSION	BG426036.1	GI:13332542
KEYWORDS	EST.	
SOURCE	human.	

```

ORANISM      Homo sapiens
REFERENCE     Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs@email.nih.gov
              Tissue Procurement: CLONTECH Laboratories, Inc.
              CDNA Library Preparation: CLONTECH Laboratories, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
              DNA Sequencing by: Incyte Genomics, Inc.
              DNA Sequencing by: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNLN at:
              http://image.lnl.nih.gov
              Plate: ULOM1345 row: n column: 03
              High quality sequence stop: 542.
FEATURES      Location/Qualifiers
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              /db_xref="taxon:9606"
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              /lab_host="DH10B (T1 phage-resistant)"
              /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
              /site_2: SfiI (ggccatattggc); 5' and
              3' adaptors were used in cloning as follows: 5' adaptor
              sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
              5'-ATCTAGAGCGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A,
              C, or G and N = A, C, G, or T). Average insert size 1.65
              kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
              by PCR. This library was enriched for full-length clones
              and was constructed by Clontech Laboratories (Palo Alto,
              CA). Note: this is a NIH_MGC Library."
BASE COUNT   192 a 213 c 212 g 181 t
ORIGIN
Query Match      64.8%; Score 256.6; DB 10; Length 798;
Best Local Similarity 79.4%; Pred. No. 2.4e-66;
Matches 317; Conservative 0; Mismatches 79; Indels 3; Gaps 1;

QY 1 atgattcacagagccaggcttctattatctgtctgtcgtatggtatctgacactgtgg 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31 ATGGTGTGCGAGACCCAGCTCTATCTCTGTTCTGTGCTGCGATCTCTGTCCTACGGG 90

QY 61 gacatttgctgtgacacagcttccagatccctgtgctgtgaagcttagagagaagggccact 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 GACATCTGTGATGACCCATCTCCAGACATCTCCCTGTGCTGTGCGGAGAGGGCCACC 150

QY 121 attagcttcaaatccagctcagagctgtgtctgaacagtagaacccgagagaactacttgct 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 ATCAACTGCAAGTCCAGCAGAGTGTTTGTGTCAGAGCTCCACCAATAGAACTACTTAAGT 210

QY 181 tgtgtaccagagaaacagagcgagcctctctaaactgtgactctactgtggcatcactaagg 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 TGGTATCCAGCACAACCAACCGAGACAGCTCTCAACTGTGCTCAATTCCTGGGCATCTAACCCGG 270

QY 241 gaacttgagggtccctgtatcgcttcagtgaggaggtgattgttggaagaagtttactctaac 300
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Db 271 GAATCCGGGGTCCCTGACGATTCAGTGTGCGAGCGGGGTGTGGGACAGATTTCCTCACCC 330

QY 301 atcagcagcttcgcagagctggaagacgttggcaatttactactcacgcgaactctata--at 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 ATCAGCAGCTGTGCAAGGCTGAAGATGTGGCACTTTATTACTCCAGCAATGTTATAGTGCT 390

QY 358 ctctacacgttcgcgacagagggaccgaaggttgaataataaa 396
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Db 391 CCTCTCACTTTCGGCGAGGAGACCAAGGTGAAGATCAAA 429

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LOCUS	AM405821	641 bp	MRNA	linear	EST 16-FEB-2000
DEFINITION	UI-HF-BL0-abp-h-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057636 5', mRNA sequence.				
ACCESSION	AM405821				
VERSION	AM405821.1	GI:6924878			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 641)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www.bio.llnl.gov/dbfp/image/image.html">www.bio.llnl.gov/dbfp/image/image.html</a> Seq primer: M13 Forward.				
FEATURES	Location/Qualifiers				
SOURCE	1..641				
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	/clone_11b="NIH_MGC_37"				
	/tissue_type="lymph"				
	/cell_type="germinal center B cells"				
	/lab_host="DH10B (LTI)"				
	/note="Vector: pUT7-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."				
BASE COUNT	159 a 178 c 163 g 141 t				
ORIGIN					
Query Match	64.6%	Score 256;	DB 9;	Length 641;	
Best Local Similarity	81.0%;	Pred. No. 3.3e-68;			
Matches 311;	Conservative 0;	Mismatched 70;	Indels 3;	Gaps 1;	
0Y	16 caggtctctatctgctctgctgcatgggattctggcacctggtggagacatgtgtgcaca	75			
Db	8 CAGGCTTCATTTCTCTGTCGTCTGGAATCTGTGGCTTACGGGGACATCTGATGACC	67			
0Y	76 cagttctccagattccctggtctgtaagcttaggagagagggccactatagctgtcaaatcc	135			
Db	68 CAGTCTCCAGATCCCTCGCTGTGTCGTGGCGAGAGGGCCACCATCAATCGAAGTCC	127			
0Y	136 agtcgaagatctctctaaagcgtagaacccgagagaaactactgtgtgtgaccagagaa	195			
Db	128 AGCCAGAGTCTTTTATACAGCTCCCAACATTAAGAACTACTTGGTGGATACGAGAAA	187			
0Y	196 ccagggcagcctccctcaaaactgctgatacttactgtgagatccactacataggaatctggtccct	255			
Db	188 CCAGGCGAGCGCTCTTAAGGTGCTCATTTACTGGGATCTACCCGGGAAATCCGGGGTCCCT	247			
0Y	256 gatgcctcagttggtcagttgagctgtggtgagacatttcaacttccatcagaagcagttcag	315			
Db	248 GACCATTTCAAGTGGCAGCGGGGTCTGGGACAGATTTTACACTTCACCATCACCATCAGCAGCCTTGAG	307			
0Y	316 gctgaagacgtgtgaggttatattacgtcaacgaacattt---taactcttaacgcttggga	372			
Db	308 GCTGAGGATGTGGCAGTTTATTACTGTGTAAGCAATATTTTAAAGTACTCTGGGAGCTTGGCC	367			

QY	373	caggggaccaggtgggaataa	396
Db	368	CAGGGACCAAGTGTGAATCAA	391
RESULT	10		
AM390292			
LOCUS	AM390292	643 bp	mrna linear
DEFINITION	CM2-ST0182-221099-023-f04 ST0182	Homo sapiens	CDNA, mRNA sequence.
ACCESSION	AM390292		
VERSION	AM390292.1	GI:6894951	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 643)		
JOURNAL	HCGP <a href="http://www.ludwig.org.br/ORESTES">http://www.ludwig.org.br/ORESTES</a> .		
COMMENT	The FAPESP/LICR Human Cancer Genome Project Unpublished (1999)		
	Contact: Simpson A.J.G.		
	Laboratory of Cancer Genetics		
	Ludwig Institute for Cancer Research		
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil		
	Tel: +55-11-2704922		
	Fax: +55-11-2707001		
	Email: <a href="mailto:asimpson@ludwig.org.br">asimpson@ludwig.org.br</a>		
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL ( <a href="http://www.ludwig.org.br/scripts/gethtml2.pl?el-CM2&amp;el2-CM2-ST0182">http://www.ludwig.org.br/scripts/gethtml2.pl?el-CM2&amp;el2-CM2-ST0182</a> )		
	221099-023:f04&t3=1999-10-22&t4=1)		
	Seq primer: puc 18 forward		
	High quality sequence start: 7		
	High quality sequence stop: 641.		
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	/dev_stage="Adult"		
	/note="Organ: stomach; Vector: puc18; Site:1: Sma1; Site:2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
BASE COUNT	162 a	173 c	162 g
ORIGIN			146 t
Query Match	64.0%	Score 253.4	DB 9
Best Local Similarity	78.9%	Pred. No. 2.1e-67	
Matches	315	Conservative	0
		Mismatches	81
		Indels	3
		Gaps	1
QY	1	atggaattcaccagccaggtctctatattgctgctgctatggtatctgycacccgtggg	60
Db	9	ATGGTGTTCACAGACCCAGGCTTCATTTCTGTTGCTCTGGATCTCTGTCCTACGAG	68
QY	61	gacatttgctgcaacagcttcacagattccctgctgctgtaagcttgagagagggccact	120
Db	69	GACATCTGTCATGACCCAGCTCTCCACATCTCCCGCTGTCCTCTGGGCGAGAGGCCACC	128
QY	121	atgactctcaaatcagatcagatcagctgctgctcacaagtagaaccgcgagagaactactgct	180
Db	129	ATCAACTGCAATCTCAGCCAGCAGATATTTTATTAACAACCTCCAAAATATAGACTACTACT	188
QY	181	tgttaccagcaaaacacagggcagcgcctctaaactcgtgacttactggtgcatccactag	240
Db	189	TGCTACGACGACAAACGAGACAGCTCTCTAAGTCGCTTTTACTGGGCAATCTACGGGG	248
QY	241	gaatctgggtccctcgatgcttcagtggtgagtgatctggagacagatttcaacttcacc	300

Db	249	AAATCCGGGGTCCCTGACCGATTCACTAGTGGCAGCGGGTCTGCGACAAATTTCACCTCACC	308
Oy	301	atcagcagctctcagagcttgaagacgttgcagttattactcagcgaacatctata--at	357
Db	309	ATCAGCAGCCTCAGAGCTGAGATGTGGCAGATTATTACTGTCAGACGATATTTAGTCA	368
Oy	358	cttcaacgcttcgacgagggagcgaagtgaggaataaa	396
Db	369	CCTCAACGTTGGCCAAAGGACCAAGGTGGAAATCAAA	407
RESULT	11		
LOCUS	BF674779	886 bp	mRNA
DEFINITION	60213793221 NIH_MGC_83 Homo sapiens cDNA	clone IMAGE:4274551 5',	
ACCESSION	BF674779		
VERSION	BF674779.1	GI:11948674	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strusberg, Ph.D.		
	Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>		
	Tissue Procurement: CLONETECH Laboratories, Inc.		
	cDNA Library Preparation: CLONETECH Laboratories, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>		
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FEATURES	High quality sequence stop: 576.		
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	/clone_lib="NIH_MGC_83"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: prostate; Vector: pDNR-LIB (Clontech);		
	/site:1: SfiI (ggcgctcgagc); Site:2: SfiI (ggcgattagcc		
	; 5' and 3' adaptors were used in cloning as follows: 5'		
	adaptor sequence: 5'-CACGGCATTATGCGC-3' and 3' adaptor		
	sequence: 5'-ATTCTAGAGCCGAGGCGCGAGATG-dT(30)BN-3',		
	(where B = A, C, or G and N = A, C, G, or T). Average		
	insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies		
	contained inserts by PCR. This library was enriched for		
	full-length clones and was constructed by Clontech		
	Laboratories (Palo Alto, CA)."		
BASE COUNT	218 a	214 c	245 g
ORIGIN	209 t		
Query Match	63.4%;	Score 251;	DB 10;
Best Local Similarity	80.2%;	Pred. NO. 1.3e-66;	
Matches	320;	Conservative 0;	Mismatches 75;
		Indels 4;	Gaps 2;
Oy	1	atgagttcaacagggccaggtctctatctatgtctgtcatatggatcttgcgaacctgtgg	60
Db	32	ATGGGTGGTGCACACCCAGGTCTTCATTTCTCTG-TGCTCTGGATCTCTGGTCTACGCG	90
Oy	61	gacatgtgtcctaacagctcttcagaattccctgctgtgaagctttgagaaagggccact	120
Db	91	GACATCGTGATGACCCAGTCTTCGAATTCCTTGCTGTGTCTCTGGGCCAGAGGCGCAC	150
Oy	121	attagctgcaaatcagttcagttcgtctctcaacagtagaaccgcgagagaactacttgct	180

	Db	151	ATCAACTGCAAGTCCAGACCGAAGTGTTTATTACACCTCCACAAATAAGACTACTTTTCT	210
Oy	181	Tggtaccagcaaaacccaggcgacctctctaactcgtgatctactggtgcatacctagt	240	
Db	211	TGGTACCAGCAGAAACCGAGGACGGCTCTTAAGTCGTCAATTACTGGGCATCTACCGG	270	
Oy	241	gaatctgggtccccctgcatcgctttagtggtgagtgatctggagcagatttccttaac	300	
Db	271	GATCCGGGGGTCCTCCAGCCGATTTCAGTGGCACCGGGGTCTGGACAGATTTCACCTCCAC	330	
Oy	301	atcacgagctctcaagctcgaagaactggtgcagtttatctgcacgcaaatctta--tat	357	
Db	331	ATTCACAGCGCTCCAGCGCTGAAGAATGTGCCAGTTTATTACTGTGCACATATTATAGTACT	390	
Oy	358	cttacacgtctcgacaaggggaccaagtlgtgaataaaa	396	
Db	391	CCTCAGACGTTCTGGCCAAGGACCAAGGTGGAATCAAA	429	
RESULT 12				
BG542772		633 bp	mRNA	linear EST 03-APR-2001
LOCUS	602571534P1 NIH_MGC_77	Homo sapiens	cDNA clone IMAGE:4695873	5'
DEFINITION			mRNA sequence.	
ACCESSION	BG542772			
VERSION	BG542772.1	GI:13535005		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	1 (bases 1 to 633)			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)			
	Contact: Robert Strausberg, Ph.D. Email: cgapbs-femail.nih.gov Tissue Procurement: Clontech Laboratories, Inc. CDNA Library Preparation: Clontech Laboratories, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: L1CM1522 row: c column: 10 High quality sequence stop: 615. Location/Qualifiers			
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	/lab_host="DH10B (T1 phage-resistant)"			
	/note="Organ: lung; Vector: pDMR-LIB (Clontech); Site: 1: SfiI (ggcgccctggccc); Site: 2: SfiI (ggccattatggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATTTATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCCGCGCCGACATG-drr(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."			
BASE COUNT	148 a 180 c 165 g 140 t			
ORIGIN				
	Query Match	62.9%	Score 249.2	DB 10: Length 633;
	Best Local Similarity	78.2%	Pred. No. 4.1e-66;	
	Matches 313; Conservative	0;	Mismatches 83;	Indels 4; Gaps 1;
Oy	1	atggattacagcgccaggttctatattgtcgcgcgtatggtatctcgacacctgtgg	60	

Db 32 ATGGTCTTCAGAGACCAGGCTTTCATTTCTGCTGCTGATCTGCTACGGG 91  
Oy 61 gacattgtctgacacagcttcacagatccctggtgtgaagcttaagaagaagggccact 120  
Db 92 GACATGCTGATGACCAAGTCTCCAGACTCCCTGCTGTCTGTGGCGAGAGGCGCACC 151  
Oy 121 attagctgaataaccagtaagctgtctcaacagtagaaccggaagaactactgtgct 180  
Db 152 ATCAGCTGCAGATCCAGACAGAGTGTATACCGCTCCAAACAAATAGGAACCTTAGCT 211  
Oy 181 tggtagcagaagaagaacaggagcagctccttaacactgtatctactgtggacactaagg 240  
Db 212 TGTATACACAGAAACACAGACAGCCTCTACCTCTCATTAATGAGGCGCTTACCGG 271  
Oy 241 gaatcgggggtccctgactgactgagtgagatctgggagcaattcactcacc 300  
Db 272 GGAATCCGGGGTCCCTTACCGCATTCAGTGGCAGCGGATCTGGACAGATTTCTACCTCACC 331  
Oy 301 atcagcagctctgagcgtgaagaagctgagcttattactgacagcaatcct---ataa 356  
Db 332 ATCAGAGAGCTGCAGGCTGAAGATGTGCGCATTCATTACGTGACGAATTTTTCATTAC 391  
Oy 357 tcttaacagcttcgagcaggaggacaaagtggaataaaa 396  
Db 392 TCCGTACACTTTCGGCCAGGAGACCAAGCTGAGATCAAA 431

RESULT 13  
AM406572 508 bp mRNA linear EST 16-FEB-2000  
LOCUS UI-HF-BL0-acu-g-10-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
DEFINITION IMAGE:3060307 5', mRNA sequence.  
ACCESSION AM406572  
VERSION AM406572.1 GI:6925629  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 508)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/db/ftp/image/image.html  
Seq primer: M13 Forward.  
Location/Qualifiers  
1..508  
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/lab\_host="DH10B (LTI)"  
/note="Vector: pT73-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaudo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 115 a 139 c 126 g 128 t

Query Match 62.5%; Score 247.6; DB 9; Length 508;  
Best Local Similarity 79.0%; Pred. No. 1.2e-65;  
Matches 308; Conservative 0; Mismatches 79; Indels 3; Gaps 1;  
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Db 10 CAGCCAGAGCTCTTCATTTCTGTTGCTCTGATCTCTGCTGCTGAGGAGCATCGTG 69  
Oy 70 ctgacacagctcagatccctgctgctgtaagcttagagaagaaggccactaagctgc 129  
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Oy 130 aaatcagtcagtgctgtctcaacagtagaaccggaagaactactgtgctgtgacag 189  
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Db 190 CTGAAACAGAGACAGCCTCTTAAGATGATCATTTACTGGGCAATCAACCGGAAATCGGG 249  
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Db 250 GTCCCTGACCGATTCACTGAGTGGCAGCGGCTGGACAGATTTTCTCTACATCAGCAGC 309  
Oy 310 ctgacagctgaagaagctgagcttattactgacagcaatctataatct---tacag 366  
Db 310 CTCAGAGCTGAAGATGTGGCAGTTTATTTACTGTGACGAATATCATGTATTCGTACAGT 369  
Oy 367 ttcggaacagaggacaaagtggaataaaa 396  
Db 370 TTTGGCCAGGAGGAGCAAGCTGAGATCAAA 399

RESULT 14  
BG686522 819 bp mRNA linear EST 01-MAY-2001  
LOCUS 602637474F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4765027 5',  
DEFINITION mRNA sequence.  
ACCESSION BG686522  
VERSION BG686522.1 GI:13917919  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 819)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LNCM1623 row: d column: 20  
High quality sequence stop: 818.  
Location/Qualifiers  
1..819  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4765027"  
/clone\_1lb="NIH\_MGC\_48"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pORF7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(5). Size-selected >500bp







GenCore version 4.5  
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OK nucleic - nucleic search, using sw model

Run on: August 26, 2002, 16:19:48 ; Search time 266.46 Seconds

(without alignments)  
2551.595 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atgattcacaggcccaaggt.....ggaccacaagtggaaataaa 396

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N.Geneseq\_032802:\*

1: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:\*  
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11: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT:\*  
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21: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	396	100.0	396	21	AAA59695
2	360.8	91.1	396	21	AAA59693
3	340	85.9	480	10	AAAN1663
4	332	83.8	952	16	AAO94036
5	301.4	76.1	439	18	AAT60729
6	301.4	76.1	439	18	AAT60730
7	298.2	75.3	399	15	AAO66845
8	293.6	74.1	402	18	AAT43415
9	288.6	72.9	399	17	AAO74067

10	288.6	72.9	439	18	AAT60734	CDNA encoding wild
11	286.8	72.1	438	17	AAT34152	Monoclonal antibody
12	285.4	72.1	439	18	AAT72268	Chimeric Mab 15 PC
13	285.4	72.1	460	18	AAT72238	Mouse Mab 15 light
14	283.2	71.5	342	20	AAAX4465	Mouse Mab 6A4 light
15	279.8	70.7	1443	15	AAO62958	Glycophorin antio
16	279	70.5	427	20	AAZ32779	Murine monoclonal
17	279	70.5	8068	20	AAZ32781	PKN100 F19 chimeri
18	278.6	70.4	748	21	AAZ28962	Human anti-glycoph
19	277.8	70.2	747	19	AAV36237	Human od ScFv DJM wh
20	275.8	69.6	870	15	AAO62956	Glycophorin antio
21	275.2	69.5	660	14	AAO53430	Sequence encoding
22	270.8	68.4	330	19	AAV29839	Anti-DNA IL/TM (H2
23	270.6	68.3	864	20	AAV72072	Fusion protein PIC
24	270.6	68.3	2019	20	AAV72059	Plasmid pMG4/55.1s
25	270.6	68.3	2025	20	AAV72064	Fusion protein PNG
26	267.2	67.5	336	20	AAAX4588	Mouse Mab 6A4 muta
27	267.2	67.5	1701	13	AAO30919	pmR1006 insert.
28	267.2	67.5	1701	13	AAO30920	Vector pmR1007.
29	264.4	66.8	404	22	AAE81911	Anti-CA125 bifunct
30	261.4	66.0	400	9	AAV80499	Encodes V region o
31	260.8	65.9	511	20	AAV86720	EST clone AY241.
32	257.4	65.0	398	15	AAO66699	DREG-200 Ab light
33	257.4	65.0	798	14	AAO34842	Encodes V kappa reg
34	255.2	64.4	423	20	AAAX9025	Human monoclonal a
35	255	64.4	1033	22	AAAS00145	Human colon cancer
36	253.6	64.0	463	21	AAO98443	Human colon cancer
37	250.2	63.2	407	13	AAO26047	V-region of L-chain
38	248.6	62.8	402	16	AAT00780	E-selectin-specifi
39	248.6	62.8	8068	20	AAZ32784	PKN100 human resha
40	248.2	62.7	344	17	AAO30900	Insert pmR1003.
41	247	62.4	5703	13	AAT34110	Anti-IL-5 humanise
42	247	62.4	5703	19	AAV03504	Plasmid pCNI15H2LC
43	244.8	61.8	744	20	AAV77243	Mouse scFv fragmen
44	244.8	61.8	774	24	AAV97144	P5-23 single chain
45	244.8	61.8	1515	24	AAV97148	3B10xP5-23 bispect

#### ALIGNMENTS

RESULT	1
ID	AAA59695 standard; DNA: 396 BP.
AC	AAA59695;
XX	XX
DT	14-NOV-2000 (first entry)
DE	DNA encoding light chain variable region of humanised 3S1 antibody.
XX	XX
XX	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW	autoimmune disease; infectious disease; inflammatory disorder;
KW	systemic lupus erythematosus; diabetes mellitus; insulin; asthma;
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW	multiple sclerosis; transplant rejection; proliferative disease;
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome; ss.
XX	XX
OS	Synthetic.
OS	Mus sp.
OS	Homo sapiens.
XX	XX
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..396
FT	/tag= a
FT	/product= "light chain variable region of 3D1 antibody"
FT	/note= "no termination codon given"
FT	1..60
FT	/tag= b
FT	mat_peptide
FT	61..396
FT	/tag= c
XX	XX

PN WO20047625-A2.  
 XX 17-AUG-2000.  
 XX  
 PE 09-FEB-2000; 2000WO-US03303.  
 XX  
 PR 12-FEB-1999; 99US-0249011.  
 PR 24-JUN-1999; 99US-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 DR WPI; 2000-524532/47.  
 DR P-PSDB; AAB07966.  
 XX  
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 PS Example 3; Fig 2B; 162pp; English.  
 XX  
 CC The present sequence encodes the light chain variable region of the  
 CC humanised murine antibody 3D1. The antibody has a binding specificity to  
 CC B7 molecules. The antibody is used to construct humanized  
 CC immunoglobulins, which comprise an antigen binding region of non-human  
 CC origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 SQ Sequence 396 BP; 100 A; 96 C; 104 G; 96 T; 0 other;

Query Match 100.0%; Score 396; DB 21; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-119;  
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggatcacaagccaggtcttatatgctgcgtgctatggatctgacccctgtgg 60  
 DB 1 atggatcacaagccaggtcttatatgctgcgtgctatggatctgacccctgtgg 60  
 QY 61 gacatgtgctgacacagctccagatccctgcgtgctgaagcttaagagaagggcact 120  
 DB 61 gacatgtgctgacacagctccagatccctgcgtgctgaagcttaagagaagggcact 120  
 QY 121 attagctgcaaatccaagctcagctcgtcctcaacagtagaaccgcagagaactacttgct 180  
 DB 121 attagctgcaaatccaagctcagctcgtcctcaacagtagaaccgcagagaactacttgct 180  
 QY 181 tgggtccacaagaagaacagggagcagcctctaactgctatctactgagcattccactaag 240  
 DB 181 tgggtccacaagaagaacagggagcagcctctaactgctatctactgagcattccactaag 240  
 QY 241 gaatctggggtccctgcatgctcagctgagctgagatcctggagacagattccactccacc 300  
 DB 241 gaatctggggtccctgcatgctcagctgagctgagatcctggagacagattccactccacc 300  
 QY 301 atcagcagctctgcaggtctgaagaacgttgagcttattactgacgcaactctataactt 360  
 DB 301 atcagcagctctgcaggtctgaagaacgttgagcttattactgacgcaactctataactt 360  
 QY 361 tacagcttcgacagggagacaaagtggaaataaaa 396  
 DB 361 tacagcttcgacagggagacaaagtggaaataaaa 396

RESULT 2  
 AAA59693  
 ID AAA59693 standard; DNA; 396 BP.  
 XX  
 AC AAA59693;  
 XX  
 DT 14-NOV-2000 (first entry)  
 XX  
 DE Nucleotide sequence of light chain variable region of 3S1 antibody.  
 XX  
 KW Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;  
 KW autoimmune disease; infectious disease; inflammatory disorder;  
 KW systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;  
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;  
 KW multiple sclerosis; transplant rejection; proliferative disease;  
 KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;  
 KW aplastic anaemia; myeloid dysplasia syndrome; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key location/Qualifiers  
 FT CDS 1..396  
 FT /\*tag= a  
 FT /product= "light chain variable region of 3D1 antibody"  
 FT /note= "no termination codon given"  
 FT sig\_peptide 1..60  
 FT mat\_peptide 61..396  
 FT /\*tag= b  
 FT /\*tag= c  
 XX  
 WO20047625-A2.  
 XX  
 17-AUG-2000.  
 XX  
 09-FEB-2000; 2000WO-US03303.  
 XX  
 12-FEB-1999; 99US-0249011.  
 PR 24-JUN-1999; 99US-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 DR WPI; 2000-524532/47.  
 DR P-PSDB; AAB07964.  
 XX  
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 PS Example 1; Fig 1B; 162pp; English.  
 XX  
 CC The present sequence encodes the light chain variable region of the  
 CC murine antibody 3D1. The antibody has a binding specificity to B7  
 CC molecules. The antibody is used to construct humanized immunoglobulins,  
 CC which comprise an antigen binding region of non-human origin and a  
 CC portion of a human immunoglobulin. The humanized immunoglobulins are  
 CC useful for treating autoimmune diseases, infectious diseases,  
 CC inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 SQ Sequence 396 BP; 98 A; 97 C; 104 G; 97 T; 0 other;

Query Match 91.1%, Score 360.8; DB 21; Length 396;  
 Best Local Similarity 94.4%; Pred. No. 7.9e-108;  
 Matches 374; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 1 atggattacagggccaggtcttattatgtctgctgatagtatctggaccctgtgg 60  
 |||||  
 Db 1 atgattacagggccaggtcttattatgtctgctgatagtatctggaccctgtgg 60  
 OY 61 gacattgtgctgacacagcttccattccctgtgctgaagcttagagagagggccact 120  
 |||||  
 Db 61 gacattgtgctgacacagcttccattccctgtgctgaagcttagagagagggccact 120  
 OY 121 attagctgcaaatccacagtcagtcgtctcaacagtagaacccgagagaactacttggct 180  
 |||||  
 Db 121 atgagctgcaaatccacagtcagtcgtctcaacagtagaacccgagagaactacttggct 180  
 OY 181 tggtaaccagcagaacccagggcagcctcctaactgctgatacttctggcaccactagg 240  
 |||||  
 Db 181 tggtaaccagcagaacccagggcagcctcctaactgctgatacttctggcaccactagg 240  
 OY 241 gaattcgggtccctgatactgctcagtcagtcagtcgagacagattccactccacc 300  
 |||||  
 Db 241 gaattcgggtccctgatactgctcagtcagtcagtcgagacagattccactccacc 300  
 OY 301 atcagcagctcgcagagcgtcgaagacgtgagcttattactcagcgaactctataactt 360  
 |||||  
 Db 301 atcagcagctcgcagagcgtcgaagacgtgagcttattactcagcgaactctataactt 360  
 OY 361 tacacgttcgacagcagggagcgaagctggaataaaaa 396  
 |||||  
 Db 361 tacacgttcgacagcagggagcgaagctggaataaaaa 396

RESULT 3  
 AAN91663  
 ID AAN91663 standard; DNA; 480 BP.

AC AAN91663;

DT 14-MAR-1990 (first entry)

DE Light chain of monoclonal antibody 6A4.

KW Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.

FT Key Location/Qualifiers

FT CDS 37..480

FT /\*tag= a

PN EP38395-A.

PD 25-OCT-1989.

PF 12-APR-1989; 89EP-0106463.

PR 19-APR-1988; 88DE-3813023.

PA (BEHW ) BEHRINGWERKE.

PI Domdey H, Marget M, von Specht BU;

DR WPI: 1989-310861/43.

DR P-PSDB; AAP93078.

XX Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for

XX variable antibody regions.

XX Claim 1; page 6; 7pp: german.

XX The sequence has a variable and constant region. Monoclonal antibody 6A4

CC reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa.

CC It is used for therapy and diagnosis of infection, and as a carrier for

CC drugs. The antibody is IgG2a subclass.

XX SQ Sequence 480 BP; 115 A; 118 C; 135 G; 112 T; 0 other;

Query Match 85.9%; Score 340; DB 10; Length 480;  
 Best Local Similarity 91.2%; Pred. No. 5.4e-101;  
 Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 1 atggattacagggccaggtcttattatgtctgctgatagtatctggaccctgtgg 60  
 |||||  
 Db 37 atggattacagggccaggtcttattatgtctgctgatagtatctggaccctgtgg 96  
 OY 61 gacattgtgctgacacagcttccattccctgtgctgaagcttagagagagggccact 120  
 |||||  
 Db 97 gacattgtgctgacacagcttccattccctgtgctgaagcttagagagagggccact 156  
 OY 121 attagctgcaaatccacagtcagtcgtctcaacagtagaacccgagagaactacttggct 180  
 |||||  
 Db 157 atgagctgcaaatccacagtcagtcgtctcaacagtagaacccgagagaactacttggct 216  
 OY 181 tggtaaccagcagaacccagggcagcctcctaactgctgatacttctggcaccactagg 240  
 |||||  
 Db 217 tggtaaccagcagaacccagggcagcctcctaactgctgatacttctggcaccactagg 276  
 OY 241 gaattcgggtccctgatactgctcagtcagtcagtcgagacagattccactccacc 300  
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 Db 277 gaattcgggtccctgatactgctcagtcagtcagtcgagacagattccactccacc 336  
 OY 301 atcagcagctcgcagagcgtcgaagacgtgagcttattactcagcgaactctataactt 360  
 |||||  
 Db 337 atcagcagctcgcagagcgtcgaagacgtgagcttattactcagcgaactctataactt 396  
 OY 361 tacacgttcgacagcagggagcgaagctggaataaaaa 396  
 |||||  
 Db 397 cgagcgttcgctgagagcgacccagcgtggaataaaaa 432

RESULT 4  
 AAQ94036  
 ID AAQ94036 standard; CDNA; 952 BP.

AC AAQ94036;

DT 21-NOV-1995 (first entry)

DE MAB 55.1 light chain CDNA.

DE Antigen binding structure; complementarity determining region; CDR;

KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;

KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;

KW transgenic animal; transgenic plant; antibody engineering;

KW humanized antibody; immunotoxin; ss.

OS Mus sp.

FT Key Location/Qualifiers

FT CDS 16..735

FT /\*tag= a

FT sig\_peptide 16..75

FT mat\_peptide 76..732

FT /\*tag= c

PN WO9515382-A.

PD 08-JUN-1995.

PF 29-NOV-1994; 94WO-GB02610.

XX 03-JUN-1994; 94GB-0011089.

PR 03-DEC-1993; 93GB-0024819.

PA (ZENEC) ZENEC LTD.  
XX  
PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;  
PI Rose MS, Wright AF;  
XX  
DR WPI: 1995-215262/28.  
DR P-PSDB: AAR76087.  
XX  
PT Antigen binding structures containing CDRs recognising the CA55.1  
PT antigen - produced by hybridomas and host cells, for use in the  
PT diagnosis and therapy of cancer  
XX  
XX  
PS Disclosure: Fig.16; 121pp; English.  
XX  
XX Mab 55.1 (ECACC 93081901) recognises the colorectal tumor-associated  
CC antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)  
CC chains of 55.1 were isolated, and F(ab)'<sub>2</sub>, Fab, Fv, scFv or  
CC V-chain humanised 55.1 constructs have been expressed in myeloma  
CC cells and E. coli.  
XX  
XQ Sequence 952 BP; 245 A; 268 C; 215 G; 224 T; 0 other;





QY 1 atggtatcacagggccaggtcttatatgtctgtctatgttggtatctggaccctgtgg 60  
 Db 1 atggatcacagacacagaggtccctcagtcgtcctcgtggtatctgttactgttgg 60  
 QY 61 gacatgtgtctgacacagctccagatctccctgtcgtgaagcttaagagaagagccact 120  
 Db 61 gacatgtgtatgacccagctccatctctccagcgtgtgtacagcagaggaaggtcact 120  
 QY 121 attagctgcaaatccagctagaagctgtctcaacagtagaacccagagaactactgtgt 180  
 Db 121 atgagctgcaagctcagctcagctcttattatacaatgaacaaagaactactgtgcc 180  
 QY 181 tggctccagcaaaaacccagggcagcctccttaactgtctatcttactcgggcatccactaag 240  
 Db 181 tggtaaccgcaaaaacccagggcagctccttaactgtctatcttactcgggcatccactaag 240  
 QY 241 gaatctgggtccctcctatcgctcagctgagctgagctcgtgagcagaattcactccacc 300  
 Db 241 ggaatctgggtccctcctatcgctcagctgagctgagctcgtgagcagaattcactccacc 300  
 QY 301 atcagcagctcgtcagcgtgaaagcgtgagcttattactgcaagcgaactctataactt 360  
 Db 301 atcagcagctggtcagcagcagaagacgtgctgttattactgcaagcagactataactt 360  
 QY 361 tacacgttcggacaggggacccaaggtggaataaaa 396  
 Db 361 tacacgttcggagctggagccaagctggaactgaaa 396

# RESULT 9

AA074067  
ID AA074067 standard; DNA; 399 BP.

XX AA074067;

DT 02-JUN-1996 (first entry)

XX Monoclonal antibody, CB-Hep-1, light chain variable domain cDNA.

XX HBV; hepatitis B virus surface antigen; monoclonal; antibody;

KW CB-Hep-1; immunopurification; detection; hybridoma; recombinant; Fv;

KW variable; VH; HBSAg; ss.

XX OS Mus sp.

XX Location/Qualifiers

XX Key 1..399

XX CDS 1..60

XX sig\_peptide 61..399

XX mat\_peptide 61..129

XX misc\_feature 130..180

XX misc\_feature 181..225

XX misc\_feature 226..246

XX misc\_feature 247..342

XX misc\_feature 343..369

XX misc\_feature 370..399

XX misc\_feature 396

XX misc\_feature 396

XX misc\_feature 396

XX misc\_feature 396

XX misc\_feature 396

XX EP686696-A1.

XX 13-DEC-1995.

XX 09-JUN-1995; 95EP-0201535.

XX 09-JUN-1994; 94CU-0000073.

XX (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.

XX (KAMB/) KAMBEEL R W.

XX Ayala Avila MA, Canaan-Haden Frias LM, del Carmen Dominguez Horta MC;

XX Fernandez de Cossio Dorta-Duque ME, Gavilondo Cowley JVG;

XX MPI; 1996-021914/03.

XX P-PSDB; AAR85909.

XX New recombinant single chain Fv antibody fragment - useful for

XX Immuno-purificn. and detection of HBSAg

XX Claim 1; Page 19; 23pp; English.

CC AA074066 and AA074067 encode the heavy and light chain variable domains  
 CC of the murine hybridoma-derived monoclonal antibody CB-Hep-1 Fv region.  
 CC The heavy and light chain regions are used to produce a recombinant  
 CC antibody fragment having specificity for the hepatitis B virus  
 CC surface antigen (HBSAg). The recombinant antibody may be used for  
 CC immunopurification of HBSAg, in immunoassays for the detection of  
 CC HBSAg and for insolubilisation of heterologous fusion proteins  
 CC expressed in E. coli aiding their purification.

XX Sequence 399 BP; 98 A; 88 C; 101 G; 112 T; 0 other;

Query Match 72.9%; Score 288.6; DB 17; Length 399;

Best Local Similarity 84.5%; Pred. NO. 3.1e-84; Matches 337; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 atggtatcacagggccaggtcttatatgtctgtctatgttggtatctggaccctgtgg 60

Db 1 atggtatcacagggccaggtcttatatgtctgtctatgttggtatctggaccctgtgg 60

QY 61 gacatgtgtctgacacagctccagatctccctgtcgtgaagcttagagagagggccact 120

Db 61 gacatgtgtatgacacagctccatctccatctcctcagctgtgtcagcttggagagaggtgt 120

QY 121 attagctgcaaatccagctagaagctgtctcaacagtagaacccagagaactactgtgt 180

Db 121 ttgagctgcaagctcagctcagctccttattatacctaacaagaactactgtgtcc 180

QY 181 tggtaaccagagaacccagggcagcctccttaactgtcgtgaactcgtgagcagctagg 240

Db 181 tggtaaccagagaacccagggcagcctccttaactgtcgtgagcagctaggcagctagg 240

QY 241 gaatctgggtccctcctatcgctcagctgagctgagctgtgagcagaattcactccacc 300

Db 241 gattctgggtccctcctatcgctcctcagcagctgagctgtgagcagaattcactccacc 300

QY 301 atcagcagctcgtcagcgtgaaagcgtgagcttattactcggcagcgaattctata 357

Db 301 atcagcagctgtagaagctggaagaccctggcagcttattactcggcagaataataat 360

QY 358 cttaacagcttcgacaggggacccaaggtggaataaaa 396

Db 361 cgttaacagcttcgagaggggacccaagctggaataaaa 399

## RESULT 10

AA074073

ID AA074073 standard; cDNA; 439 BP.

XX AA074073;

Query Match	Best Local Similarity	72.9%	Score 288.6	DB 18	Length 439
Matches 337	Conservative 0	Mismatches 59	Indels 3	Gaps 11	
1	atgatactcagagccacaggtctctctatattgctgcgtctgatacgtgatactgacactgtgg	60			
28	atggagctcagacagctcagctctctatgtcttcctgcgtctgtgtatctgtatcctgtgg	87			
61	gacatctgtgtcagacagctctccagattccctgcgtgttaagcttaggagagagggccact	120			
88	gacatctgtgtatgacacagctctccatccctccctgcgtgtgacagcagagagagagtcact	147			
121	atgaatctcagaaatccagcttagagctgtgtctgctccacagtagaaccggagagaaactactgtgt	180			
148	atgagctctgaaagctcagtagaagctctgtgtacacagctgtagaagaaactaaagaaactactgtacc	207			

Query Match	72.4%	Score 286.8	DB 17	Length 418
Best Local Similarity	84.8%	Pred. No. 1.2e-83		
Matches 334; Conservative	0	Mismatches 57	Indels 3	Gaps 1













Db 190 TGGTACACAGAGACAGGAGGAGTCTCTAAACTGCTATGTATGGGATCCACTAGG 249  
Qy 241 gaatctggggtccctgatctcgaatgagtcgaatcggagcaatctcacc 300  
Db 250 ACATCTGGGGTCCCTGATGCTTCACAGGACAGTGATCTGGGACATTTCACTCTCACC 309  
Qy 301 atcagcagctcgaagctgaagacgtgagcttattactgacagcaatcttaactc 360  
Db 310 ATCAGCAGTGTGAGGCTTAAGACCTGGCAATTTATTACTGCAAGCAATCTTACTCTT 369  
Qy 361 tacacgttcgacagggaccacgaagtggaaataaa 396  
Db 370 CGAGCTTCGTGGAGGACACCAAGCTGGAATCAAA 405

RESULT 2  
US-08-929-856-65  
; Sequence 65, Application US/08929856  
; Patent No. 6136568

GENERAL INFORMATION:  
APPLICANT: Hatt, Andrew  
APPLICANT: Rose, Floyd  
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING  
TITLE OF INVENTION: ROLLING TEMPLATES  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LERNER, DAVID, LITTEMBERG, KRUMHOLZ &  
STREET: 600 South, Avenue West  
CITY: Westfield  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07090  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/929,856  
FILING DATE: 15-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REGISTRATION NUMBER: 33, 071  
REFERENCE/DOCKET NUMBER: ROSE 3.0-057  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 342 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..342  
US-08-929-856-65

Query Match 71.5%; Score 283.2; DB 3; Length 342;  
Best Local Similarity 90.2%; Pred. No. 6.2e-82;  
Matches 303; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 61 gacatttgctgacacagctcccaattccctgctgctgaagcttaagagagagggccact 120  
Db 1 GACATTGTGATGTACACAGTCTCCATCTCCCTGGCTGTGTCACAGCAGAGAGAGATCAGCT 60  
Qy 121 attagctgcaaatcagctcagagctcgtctcaacagtagaacccgagaaactacttgct 180  
|||

Db 61 ATGAGCTGCAAAATCCAGTCAAGCTCTGCTCAACAGTATTAACCCGAAGAAGACTTCTGGCT 120  
Qy 181 tggtaacagcaagaacaaaggagcctccttaactctgaatctcactcagggatccactagg 240  
Db 121 TGGTACACAGAGAAACACAGGAGGAGTCTCTAAACTGCTATGTATGGGATCCACTAGG 180  
Qy 241 gaatctggggtccctgatctcgaatgagtcgaatcggagcaatctcacc 300  
Db 181 GATCTGGGGTCCCTGATGCTTCACAGGACAGTGATCTGGGACATTTCACTCTCACC 240  
Qy 301 atcagcagctcgaagctgaagacgtgagcttattactgacagcaatcttaactc 360  
Db 241 ATCAGCAGTGTGAGGCTTAAGACCTGGCAATTTATTACTGCAAGCAATCTTACTCTT 300  
Qy 361 tacacgttcgacagggaccacgaagtggaaataaa 396  
Db 301 CGAGCTTCGTGGAGGACACCAAGCTGGAATCAAA 336

RESULT 3  
US-08-403-853-19  
; Sequence 19, Application US/08403853  
; Patent No. 5844094

GENERAL INFORMATION:  
APPLICANT: HUDSON, Peter J.  
APPLICANT: LAH, Maria  
APPLICANT: KORR, Alex A.  
APPLICANT: IRVING, Robert A.  
APPLICANT: ATWELL, John L.  
APPLICANT: MALBY, Robyn L.  
APPLICANT: POWER, Barbara E.  
APPLICANT: COLMAN, Peter M.  
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,853  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU93/00491  
FILING DATE: 24-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PL 4973  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29, 768  
REFERENCE/DOCKET NUMBER: 16786/189/CHAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1443 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-403-853-19



APPLICATION NUMBER: US 07/983,949  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-45  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ. ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 399 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..399  
PCT-US93-11611-1

Query Match 70.1%; Score 277.4; DB 5; Length 399;  
Best Local Similarity 82.7%; Pred. No. 4,8e-80;  
Matches 330; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 atgattccacagagccaggtcttctattatgtctgtatggtatctgtgacactgtg 60  
DB 1 ATGATTTCACAGGCCAGGTTCTTATGTACTGCTGTAAGTATCTGGAACCTGTGG 60  
QY 61 gaattgtctgaacacagttccagattccctgtgttaagcttagagagagagccact 120  
DB 61 GAACTGTGTATGTCAAGAGTCTCCATCTCCCTGCTGTCACTTGAGAGAGGTTACT 120  
QY 121 attagctgcaaatcagctgaagctgtctgccaacagtagaaccagagaaactctggct 180  
DB 121 ATGAGCTGCAAGTCCAGTCAAGAGCTTTTACTAGCTGTGTCACTTGAGAGAGGTTACT 180  
QY 181 tggtaacagcaagaacacagagcagcctcctaactgtctgatactcagggatccactag 240  
DB 181 TGGTACCAGACAGAAACAGAGGCGAGTCTCCAAACTGCTGATTACTGGGATCTACTAGG 240  
QY 241 gaattcggaggtccctgattcgtctcagtgagatgagatcggagacagattcactcacc 300  
DB 241 GAATCTGGGGTCCCTGATCGCTTCACAGGCGAGTGGGATCTGGGACAGATTTCACCTCACC 300  
QY 301 atcagaagctcgaagctgaagaacgctgagcagttattactgacggaatctta--at 357  
DB 301 ATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTATTACTGTCAACAATATTATAGCTAT 360  
QY 358 cttaacagcttcgagacagggagcaaggtggaataaaa 396  
DB 361 CCATTCACTGGCTCGCGGGGACAAAGTTGGAATAAAAA 399

RESULT 6  
US-08-403-853-15  
Sequence 15, Application US/08403853  
Patent No. 5844094

GENERAL INFORMATION:

APPLICANT: HUDSON, Peter J.  
APPLICANT: LAH, Maria  
APPLICANT: KORRT, Alex A.  
APPLICANT: IRVING, Robert A.  
APPLICANT: ATWELL, John L.  
APPLICANT: MALBY, Robyn L.  
APPLICANT: POWER, Barbara E.  
APPLICANT: COLMAN, Peter M.  
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,853  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU93/00491  
FILING DATE: 24-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PL 4973  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16786/189/CHAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ. ID NO. 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 870 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: mat.peptide  
LOCATION: 40..834  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 40..834  
US-08-403-853-15

Query Match 69.6%; Score 275.8; DB 2; Length 870;  
Best Local Similarity 89.0%; Pred. No. 2.1e-79;  
Matches 298; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 61 gaattgtctgacagatctcagattccctgtgttaagcttagagagagagccact 120  
DB 463 GAACTGTGTATGTCAAGAGTCTCCATCTCCCTGCTGTGTCACTAGAGAGAGTCACT 522  
QY 121 attagctgcaaatcagctgaagctgtctcgaacagtagaaccgagagaaactcctggct 180  
DB 121 ATGAGCTGCAAGTCCAGTCAAGAGTCTGTTCAACAGTAGAAGAACCGAAGAACTCTGAGT 582  
QY 181 tggtaacagcaagaacacagggagcagcctcctaactgtctgatactcagggatccactag 240  
DB 181 TGGTACCAGACAGAAACAGAGGCGAGTCTCCAAACCGCTGATCTAGGCGATCACTAGG 642  
QY 241 gaattcggaggtccctgattcgtctcagtgagatgagatcggagacagattcactcacc 300  
DB 241 GAATCTGGGGTCCCTGATCGCTTCACAGGCGAGTGGGATCTGGGACAGATTTCACCTCACC 702  
QY 301 atcagaagctcgaagctgaagaacgctgagcagttattactgacgcaactcttaactc 360  
DB 301 ATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTATTACTGCAAGCAATCTTATATCTT 762  
QY 361 tacaagctcggagacagggagcaaggtggaataaaa 395  
DB 763 CGGACGTTGGTGGAGGACCAAGCTGGAATAATTA 797

RESULT 7  
US-08-957-001B-4



Sequence 4, Application US/08957001B  
Patent No. 6228621  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madalo, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/957,001B  
FILING DATE: 23-OCT-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..330  
US-08-957-001B-4

Query Match 68.4%; Score 270.8; DB 4; Length 330;  
Best Local Similarity 88.8%; Pred. No. 5.9e-78;  
Matches 293; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
QY 61 gacattgtgtctacacagctccagatccctgtgctgtaagcttagagagagagaccact 120  
DB 1 GACATTGTGTATTCACAGCTCCATCCACCTTGCTGTGTACAGCAGAGAGAGGTCACCT 60  
QY 121 attagctgcaaatccagctcagctcgtctcgaacagtagaaccgagagaaactctgct 180  
DB 61 ATGAAGCTGCNAATCCAGCTCAGAGTCTGTCTCAACAGTAGAACCAGAAACTACTGGCT 120  
QY 181 tggttccacagaaacacagagggcagctcctctaaactgtctatctactcagggcatccactag 240  
DB 121 TGGTTCCACAGAAACCAAGGAGCTCTCTAAACTGCTGATCTACTAGGGCATTCACTAGG 180  
QY 241 gaattcgggggtccctgatgctctcagctgagctgagctcgtgagacagattcactctcacc 300  
DB 181 GAATCTGGGGTCCCTGATGCTTTCACAGGAGTGGATCTGGGACATTTCACTCTCACCC 240  
QY 301 atcagcagctcgcagggctggaagaagctgagcagtttacttactcagcagcaattcttaact 360  
DB 241 ATCAGCAGAGTGTCTCAGGCTGAAGACCTGCGCATTTATTACTGCAAGCAATCTTATTTCTT 300  
QY 361 tacacgttcgcagcagggagcacaagtgtgaa 390

DB 301 CGACGTTTCGTGAGGACGACACAGGCTTGAA 330  
RESULT 8  
US-09-496-301-4  
Sequence 4, Application US/09496301  
Patent No. 6248565  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madalo, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,301  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/957,001  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..330  
US-09-496-301-4

Query Match 68.4%; Score 270.8; DB 4; Length 330;  
Best Local Similarity 88.8%; Pred. No. 5.9e-78;  
Matches 293; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
QY 61 gacattgtgtgacacagcttccagatccctgtgctgtaagcttagagagagagaccact 120  
DB 1 GACATTGTGTATTCACAGTCTCCATCCACCTTGCTGTGTACAGCAGAGAGGTCACCT 60  
QY 121 attagctgcaaatccagctcagctcgtctcgaacagtagaaccgagagaaactctgct 180  
DB 61 ATGAAGCTGCNAATCCAGCTCAGAGTCTGTCTCAACAGTAGAACCAGAAACTACTGGCT 120  
QY 181 tggttccacagaaacacagagggcagctcctctaaactgtctatctactcagggcatccactag 240  
DB 121 TGGTTCCACAGAAACCAAGGAGGAGTCTCTAAACTGCTGATCTACTAGGGCATTCACTAGG 180  
QY 241 gaattcgggggtccctgatgctctcagctgagctgagctcgtgagacagattcactctcacc 300

DB 181 GAATCTGGGGTCCCTGATCGCTTCACAGGCACTGGATCGGACAGATTCTCACTCCACC 240  
QY 301 atcaacagctctcaagctgaaagcgtgagcttattctgacccaatctatactt 360  
DB 241 ATCAAGAGTGTGAGAGCTGGAAGCTTTATTACTGCAAGCAATCTTATTACTT 300  
QY 361 tacacgtctcgacaggggaccaaagctgga 390  
DB 301 CGGACGTTGCGTGAAGGCAACGAGCTGGANA 330

## RESULT 9

US-09-423-439-47  
; Sequence 47, Application US/09423439  
; Patent No. 6339070

## GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997

## INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:  
LENGTH: 864 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
US-09-423-439-47

Query Match 68.3%; Score 270.6; DB 4; Length 864;  
Best Local Similarity 86.0%; Pred. No. 1e-77;

Matches 300; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 48 tggacacctgtgggagacatgtgtcagacagctcagattccctgctgtaagctagg 107  
DB 462 TGGCGGGGATCTGACATTGACCTCTCACAGTCTCCATCTCTCCCTGGCTGTGTACACAGG 521  
QY 108 agagagggcactatagctgaatccagctcagaagctcgtcacaacagtagaaccggaga 167  
DB 522 AAGAGAAGTCCACCATAGCTGCAATCCAGTCCAGATCTCCCTCAACAGTAGAACCCGANA 581  
QY 168 gaactactgtgctgttacagcagaacacagggcagcctcctaaactgtgactactg 227  
DB 582 GAACACTTGTGCTGTGTACACAGAGACAGGCGAGTCTCTTAACCTGCTGATCTATTG 641  
QY 228 ggcattccactaaggaaatcgggggtccctgatacgtcctcagtgagtgagtgagtgag 287  
DB 642 GGCATCTACATAGACATCTGGGGTCCCTGATCGCTTCACAGCAAGTAGATCTGGACAGA 701

QY 288 ttcaactcaccatcagcagctcgaagctgaagaagctgagcttattactgacgca 347  
DB 702 TTTCACTCTCACCATTCAGAGAGTGTGACAGCTGAGACCTGCCAATTTATTACTGCAAGCA 761  
QY 348 attcataactcttacacgtctgacaggggagcgaagtgaggaataaaa 396  
DB 762 ATCTTACTCTTTCGACGCTGTGAGAGGACCAAGCTGAGATCAAA 810

## RESULT 10

US-09-423-439-31  
; Sequence 31, Application US/09423439  
; Patent No. 6339070

## GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997

## INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2019 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-423-439-31

Query Match 68.3%; Score 270.6; DB 4; Length 2019;  
Best Local Similarity 86.0%; Pred. No. 1.4e-77;

Matches 300; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 48 tggacacctgtgggagacatgtgtcagacagctcagattccctgctgtaagctagg 107  
DB 453 TGGCGGGGATCTGACATTGACCTCTCACAGTCTCCATCTCTCCCTGGCTGTGTACACAGG 512  
QY 108 agagagggcactatagctgaatccagctcagaagctcgtcacaacagtagaaccggaga 167  
DB 513 AAGAGAAGTCCACCATAGCTGCAATCCAGTCCAGATCTCTCAACAGTAGAACCCGANA 572  
QY 168 gaactactgtgctgttacagcagaacacagggcagcctcctaaactgtgactactg 227  
DB 573 GAACACTTGTGCTGTGTACACAGAGACAGGCGAGTCTCTTAACCTGCTGATCTATTG 632  
QY 228 ggcattccactaaggaaatcgggggtccctgatacgtcctcagtgagtgagtgagtgag 287  
DB 633 GGCATCTACATAGACATCTGGGGTCCCTGATCGCTTCACAGCAAGTAGATCTGGACAGA 692  
QY 288 ttcaactcaccatcagcagctcgaagctgaagaagctgagtgagtgagtgagtgag 347  
DB 693 TTTCACTCTCACCATTCAGAGAGTGTGACAGCTGAGACCTGCAAGTATTTATTACTGCAAGCA 752

QY 348 attctataatctttaaactgctcgagacagggagaccaggtggaataa 396  
DB 753 ATCTTATACCTCTCGACGCTTGGGTGAGGACCAAGCTCGAGATCAAA 801

## RESULT 11

US-09-423-439-37  
Sequence 37, Application US/09423439  
Patent No. 6339070  
GENERAL INFORMATION:  
APPLICANT: EMERY, Stephen Charles  
BLAKEY, David Charles  
TITLE OF INVENTION: CHEMICAL COMPOUNDS  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Winthrop, L.L.P.  
STREET: 1100 New York Ave., N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: MS WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/423,439  
FILING DATE: 09-NO. 6339070-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01294  
FILING DATE: 05-MAY-1998  
APPLICATION NUMBER: GB 9709421.3  
FILING DATE: 10-MAY-1997  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2025 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-423-439-37

Query Match 68.3%; Score 270.6; DB 4; Length 2025;  
Best Local Similarity 86.0%; Pred. No. 1.4e-77;  
Matches 300; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 48 tggcaccctgtgggacattgtgctgacacagcttcacagattccctgctgtaagcttag 107  
DB 453 TGGCGCGGATCGATCGATGAGCTCTCACAGTCTCCATCCCTGGCTGTGCAGAGG 512  
QY 108 agagaggggcacattagctgcaaatccagctgagagctgcttaaacagtagaacccgaga 167  
DB 513 AAGAGAGGTCACCATGAGCTGCAAAATCCAGTCCAGTCTCTCAACAGTAGAACCCGAAA 572  
QY 168 gaactactggtctgtgtacacagagaacacagggcagccctcctaactgtgtactag 227  
DB 573 GAACTACTTGGCTTGGTACACAGCAGACACAGGAGCTCTCTAAACTGTGATCTATTG 632  
QY 228 ggcattcactaggaattcgggggtccctgataccttcagctcagtgagtgagctggaaga 287  
DB 633 GGCATCACTAGAGACATCTGGGGTCCCTGATCCCTTCACAGGAGAGTGCATCTGGACAGA 692  
QY 288 tttaacttcacacatcagcagctgcaagctggaagcagctggaagcttataactgcaagca 347  
DB 693 TTTCACTCTCACACATCAGAGTGTGCAGGCTGAAGACCTGGCAATTATTACTGCAAGCA 752  
QY 348 attctataatctttaaactgctcgagacagggagaccaggtggaataa 396  
DB 753 ATCTTATACCTCTCGACGCTTGGGTGAGGACCAAGCTCGAGATCAAA 801

DB 753 ATCTTATACCTCTCGACGCTTGGGTGAGGACCAAGCTCGAGATCAAA 801

## RESULT 12

US-08-929-856-188  
Sequence 188, Application US/08929856  
Patent No. 6136568  
GENERAL INFORMATION:  
APPLICANT: Hiatt, Andrew  
Hiatt, Floyd  
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LERNER, DAVID, LITTEBERG, KRUHOLZ &  
STREET: 600 South, Avenue West  
CITY: Westfield  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07090  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/929,856  
FILING DATE: 15-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REGISTRATION NUMBER: 33,071  
REFERENCE/DOCKET NUMBER: ROSE 3.0-057  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 342 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..342  
US-08-929-856-188

Query Match 67.5%; Score 267.2; DB 3; Length 342;  
Best Local Similarity 87.2%; Pred. No. 8.6e-77;  
Matches 293; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 61 gacattgtgtgacacagcttcacagattccctgctgtaagcttagaagagggccact 120  
DB 1 GACATTGTGATGTACAGCTGTCCATCTCCCTGGCTGTGCAGGAGAGAGTCTACT 60  
QY 121 attagctgaatccacagctgagctgctcaacagtagaacccgaggaactactgtgct 180  
DB 61 ATGAGCTGCAAAATCCACTGAGGCTGCTCAACAGTAAACCCGAAGAACTTCTTGCT 120  
QY 181 tggtaacagagaacacagggcagccctcctaactgctgatactactggtgatacactag 240  
DB 121 TGGTACACAGAGAAGACGAGGAGTCTCTAAACTGTGATCTACTTGCATCCACTAGG 180  
QY 241 gaattcgggggtccctgataccttcagctcagtgagctggaagcttcaactcacc 300  
DB 181 GAACTCTGGGGTCCCTGTATCTCTTCACAGGAGTGCATCTGGAGATTTCACCTCACC 240  
QY 301 atagcagcttcgagcgtggaagcgttggcagcttattactgcaagcagcttataact 360  
DB 241 ATCAGCAGTGTGACGCTGAAGACCTGGCAGTTATTACTGCCATTAATTTCTTAATCTT 300





Search completed: August 26, 2002, 16:15:01  
Job time: 4250 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2002, 14:59:37 ; Search time 25.86 Seconds

(without alignments)  
490.479 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681

Sequence: 1 MDSQAQVILLLLMVSGTGC.....YCTOSYNYTFSGGTKEIK 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	87.5	133	2 PS0023	Ig kappa chain pre
2	558.5	82.0	134	1 K4HU17	Ig kappa chain pre
3	558	81.9	120	2 G33932	Ig kappa chain pre
4	553.5	81.3	134	2 S49531	anti-Sm antibody V
5	552	81.1	133	1 K4HU1	Ig kappa chain pre
6	542.5	79.7	138	2 S26040	Ig kappa chain pre
7	541.5	79.5	145	2 PL0014	Ig kappa chain pre
8	539.5	79.2	134	2 PC1214	Ig kappa chain pre
9	536.5	78.8	135	2 S38807	Ig light chain V-J
10	536	78.7	138	2 A53261	Ig kappa chain pre
11	535.5	78.6	129	2 S40347	Ig kappa chain - h
12	532.5	78.2	240	2 S06084	Ig kappa chain pre
13	528.5	77.6	132	2 S46373	Ig kappa chain V-J
14	515.5	75.7	134	2 S21917	Ig kappa chain V r
15	515	75.6	121	1 K4HU	Ig kappa chain pre
16	510	74.9	113	2 PT0407	Ig light chain V r
17	506.5	74.4	120	2 S51147	antibody light cha
18	506.5	74.4	124	2 S40364	Ig kappa chain - h
19	506	74.3	112	2 S43103	Ig kappa chain V-J
20	502.5	73.8	113	2 S34002	Ig kappa chain V r
21	500.5	73.5	136	2 A49137	Ig kappa chain pre
22	497.5	73.1	114	1 K4HULN	Ig kappa chain V-I
23	494	72.5	112	2 PL0265	Ig kappa chain V r
24	493.5	72.5	129	2 S40329	Ig kappa chain V r
25	492	72.2	113	2 PT0408	Ig light chain V r
26	490.5	72.0	113	2 S30520	Ig kappa chain V r
27	482	70.8	102	2 S41393	Ig kappa chain V r
28	480	70.5	113	2 PH1047	Ig light chain V r
29	476.5	70.0	113	2 S34003	Ig kappa chain V r

30	475	69.8	103	2 PH1052	Ig light chain V r
31	473.5	69.5	111	2 S03304	Ig kappa chain V r
32	473.5	69.5	114	2 S44116	Ig kappa chain V-J
33	473.5	69.5	114	2 S44119	Ig kappa chain V-J
34	471	69.2	104	2 PH1101	Ig light chain V r
35	470.5	69.1	113	2 S30523	Ig kappa chain V r
36	470	69.0	104	2 PH1102	Ig light chain V r
37	467	68.6	103	2 PH1051	Ig light chain V r
38	466	68.4	104	2 PH1104	Ig light chain V r
39	464	68.1	103	2 PH1050	Ig light chain V r
40	462.5	67.9	113	2 PL0263	Ig kappa chain V r
41	460	67.5	101	2 PH1046	Ig kappa chain V r
42	457	67.1	104	2 PH1103	Ig light chain V r
43	452.5	66.4	113	2 PL0264	Ig light chain V r
44	452.5	66.4	214	2 S68212	Ig kappa chain (Ma
45	452	66.4	106	2 A49138	IgA kappa rheumato

## ALIGNMENTS

## RESULT 1

PS0023

Ig kappa chain precursor V region (6A4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000

C:Accession: PS0023

R:Margel, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.

Gene 74: 335-345, 1988

A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains

A:Reference number: PS0023; MUID:89237225

A:Accession: PS0023

A:Molecule type: mRNA

A:Residues: 1-133 <MAR>

A:Experimental source: strain BALB/c

A:Note: the amino-terminal four residues of the mature protein were directly sequence

C:Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aer

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>

F:36-116/Domain: immunoglobulin homology <IMH>

Query Match Best Local Similarity 87.5%; Score 596; DB 2; Length 133;

Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Oy 1 MDSQAQVILLLLMVSGTGDIVLTQSPDSLAVSIGERATISCKSSQSLNSRTRENTLA 60

Db 1 MDSQAQVILLLLMVSGTGDIVMSQSPSLAVSAGEKVTMSCKSSQSLNSITRKPLA 60

Oy 61 WYQKPGQPKLLTYWASTRESGVDPREGSGSGGDFLTSSLOAEVAVYYCQSNL 120

Db 61 WYQKPGQPKLLTYWASTRESGVDPREGSGSGGDFLTSSLOAEVAVYYCQSNL 120

Oy 121 YTFGSGTKEIK 132

Db 121 RTFGSGTKEIK 132

RESULT 2

K4HU17

Ig kappa chain precursor V-IV region (B17) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 21-Jan-2000

C:Accession: A01905

R:Marsh, P.; Mills, F.; Gould, H.

Nucleic Acids Res. 13, 6531-6544, 1985

A:Title: Detection of a unique human Kappapraty germline gene by a cloned cDNA probe.

A:Reference number: A01905; MUID:86041854

A:Accession: A01905

A:Molecule type: mRNA





```

Oy      4  QAOVILLILLIWSGTCGDIVLTOSPDLSIAVLGEATATISCKSSOSLISRTENTYLAWQ 63
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4  QVOVFISLLIMISGAYDIWMTQSPDSLAVSLGERATINCSSQSVLYSNKNKNTIAMIQ 63
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy      64  QKRGQPKLLIYWASTRESGVDPDRFSGSGSGTDEFTLTITSSLOAEDVAVYYCTQSYNLTYF 123
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      64  QKRGQPKLLIYWASTRESGVDPDRFSGSGSGTDEFTLTITSSLOAEDVAVYYCQOYDITPTF 123
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy      124  GGGTKVEIK 132
      1  | | | | | | | |
Db      124  GGGTKVEIK 132
      1  | | | | | | | |

RESULT 6
S26040
Ig kappa chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000
C:Accession: S26040; S78098
R:Okamoto, M.; Honjo, T.
Nucleic Acids Res. 18, 1895, 1990
A:Title: Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoan-
A:Reference number: S09216; MUID:90245585
A:Accession: S26040
A:Molecule type: DNA
A:Residues: 1-138 <OK>
A:Cross-references: EMBL:X51742
A:Note: The authors translated the codon AGC for residue 107 as Thr and AGT for residue
R:Okamoto, M.
submitted to the EMBL Data Library, February 1990
A:Reference number: S78098
A:Accession: S78098
A:Molecule type: DNA
A:Residues: 1-87, 'N', 89-138 <OK>
A:Cross-references: EMBL:X51742; NID:g52697; PIND:CA36032.1; PID:g52698
C:Genetics:
A:Introns: 22/1
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F:1-25/DNA: signal sequence #status predicted <Sig>
F:26-138/Product: Ig kappa chain (fragment) #status predicted <Mat>
F:41-121/DNA: immunoglobulin homology <IMM>

Query Match      79.7%; Score 542.5; DB 2; Length 138;
Best Local Similarity 75.2%; Pred. NO. 4.4e-39;
Matches 103; Conservative 17; Mismatches 12; Indels 5; Gaps 1;

Oy      1  MDSQAQVILLILLIWSG-----TCGDIVLTQSPDSLAVSLGERATISCKSSOSLISRTNR 55
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  MDSQAQVILLILLIWSGEEKRSTCGDIVMSQSPSSLIVSVEKVTMCKSSOSLISNNQ 60
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy      56  ENYLAIVQKPGQPKLLIYWASTRESGVDPDRFSGSGSGTDEFTLTITSSLOAEDVAVYYCT 115
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61  KNYLAIVQKPGQSPKLLIYWASTRESGVDPDRFSGSGSGTDEFTLTITSSVAKEDLAIVYFCQ 120
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy      116  OSYNLYTFGGTKVEIK 132
      1  | | | | | | | | | | | | | |
Db      121  QYSLTFGAGTKLEIK 137
      1  | | | | | | | | | | | | | |

RESULT 7
PL0014
Ig kappa chain precursor V region (F6-3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0014
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Dimmis, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: PL0011; MUID:88142865
A:Accession: PL0014
A:Molecule type: mRNA

```

A:Residues: 1-145 <CHP>  
A:Experimental source: cell line F6-3  
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-134/Product: Ig heavy chain V region (C11) #status predicted <MAT>  
F:36-116/Domain: immunoglobulin homology <IMM>  
F:44-60/Region: complementarity-determining 1  
F:76-82/Region: complementarity-determining 2  
F:115-123/Region: complementarity-determining 3  
F:135-145/Domain: constant region (fragment) #status predicted <COR>

Query Match 79.5%; Score 541.5; DB: 2; Length 145;  
Best Local Similarity 77.6%; Pred. No. 5.7e-39;  
Matches 104; Conservative 18; Mismatches 9; Indels 3; Gaps 2;

OY 1 MDSQAOVILLLILMWSTGCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60  
DB 1 MDSQAOVILLLILMWSTGCGDIVMSQSPSLAVSGEAVTMSQSSQSLIYNSNQKNFLA 60  
OY 61 WYQOKPGQPKLLIYMASTRSGVDPDRFSGSGSGTDFLLTISLQAEVAVYYCTQSYNL 120  
DB 61 WYQOKPGQPKLLIYMASTRSGVDPDRFTGSGSGTDFLLTISYKAEADLAVYYCQOYYNS 119  
OY 121 Y--TFGGGKVEIK 132  
DB 120 YPLTRGSGTKLEMK 133

RESULT 8  
PC1214  
Ig kappa chain precursor V region (Mab H8) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PC1214  
R:Hong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; K  
Gene 121, 331-335, 1992  
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a  
A:Reference number: PC1213; MUID:93077049  
A:Accession: PC1214  
A:Molecule type: mRNA  
A:Residues: 1-134 <HON>  
A:Cross-references: GB:M98042; NID:g196749; PIDN:AAA38777.1; PID:g196750  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-134/Product: Ig light chain V region #status predicted <MAT>  
F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 539.5; DB: 2; Length 134;  
Best Local Similarity 78.9%; Pred. No. 7.7e-39;  
Matches 105; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

OY 1 MDSQAOVILLLILMWSTGCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60  
DB 1 MDSQAOVILLLILMWSTGCGDIVMSQSPSLAVSGEAVTMSQSSQSLIYNSIQKNFLA 60  
OY 61 WYQOKPGQPKLLIYMASTRSGVDPDRFSGSGSGTDFLLTISLQAEVAVYYCTQSYNL 120  
DB 61 WYQOKPGQPKLLIYMASTRSGVDPDRFTGSGSGTDFLLTISYKAEADLAVYYCQOYYNY 120  
OY 121 -YTFGGGKVEIK 132  
DB 121 PSTFGGTYLEIK 133

RESULT 9  
S38807  
Ig light chain V-J region - mouse  
C:Species: Mus musculus (house mouse)







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:05:39 ; Search time 15.59 Seconds

(without alignments)  
327.837 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681

Sequence: 1 MDSQAQVILLILLMWSTGTCG.....YCTGSYNLTYGCGTKVEIK 132

Scoring table: BIOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571.5	83.9	134	KV4C_HUMAN	P06314 homo sapien
2	552	81.1	133	KV4B_HUMAN	P06313 homo sapien
3	515	75.6	121	KV4A_HUMAN	P01632 homo sapien
4	502.5	73.8	114	KV4A_HUMAN	P01625 homo sapien
5	446	65.5	129	KV3H_HUMAN	P04207 homo sapien
6	442	64.9	129	KV3L_HUMAN	P18135 homo sapien
7	440	64.6	129	KV3M_HUMAN	P18136 homo sapien
8	418	61.4	133	KV2E_HUMAN	P06310 homo sapien
9	416.5	61.2	129	KV1U_HUMAN	P04431 homo sapien
10	409.5	60.1	128	KV3K_HUMAN	P06311 homo sapien
11	408.5	60.0	131	KV3I_MOUSE	P01651 mus musculu
12	408.5	60.0	132	KV3F_MOUSE	P01658 mus musculu
13	396	58.1	115	KV3I_HUMAN	P04433 homo sapien
14	394.5	57.9	116	KV3J_HUMAN	P04434 homo sapien
15	394	57.9	110	KV3P_MOUSE	P01658 mus musculu
16	393.5	57.8	136	KV5B_MOUSE	P01674 mus musculu
17	392.5	57.6	149	KV5A_MOUSE	P01673 mus musculu
18	384	56.4	109	KV3B_HUMAN	P01620 homo sapien
19	384	56.4	109	KV3F_HUMAN	P01624 homo sapien
20	383	56.2	109	KV3D_HUMAN	P01622 homo sapien
21	382.5	56.2	111	KV3K_MOUSE	P01655 mus musculu
22	382.5	56.2	111	KV3O_MOUSE	P01657 mus musculu
23	381	55.9	109	KV3E_HUMAN	P01623 homo sapien
24	380.5	55.9	117	KV2E_HUMAN	P06309 homo sapien
25	380.5	55.9	108	KV1M_HUMAN	P01605 homo sapien
26	380.5	55.9	111	KV3J_MOUSE	P01654 mus musculu
27	379.5	55.7	111	KV3U_MOUSE	P01673 mus musculu
28	377.5	55.4	111	KV3H_MOUSE	P01660 mus musculu
29	375.5	55.1	111	KV3N_MOUSE	P01666 mus musculu
30	374.5	55.0	111	KV3O_MOUSE	P01669 mus musculu
31	374.5	55.0	111	KV3R_MOUSE	P01670 mus musculu
32	374.5	55.0	111	KV3S_MOUSE	P01671 mus musculu
33	373.5	54.8	115	KV2A_HUMAN	P01614 homo sapien

34	370	54.3	109	1	KV3G_HUMAN	P04206 homo sapien
35	368.5	54.1	117	1	KV1J_HUMAN	P01602 homo sapien
36	368.5	54.1	129	1	KV1X_HUMAN	P04432 homo sapien
37	367	53.9	108	1	KV3A_HUMAN	P01619 homo sapien
38	366.5	53.8	108	1	KV1V_HUMAN	P04430 homo sapien
39	366.5	53.8	111	1	KV3D_MOUSE	P03977 mus musculu
40	366.5	53.8	111	1	KV3J_MOUSE	P01652 mus musculu
41	366.5	53.8	111	1	KV3T_MOUSE	P01672 mus musculu
42	366.5	53.8	114	1	KV1A_MOUSE	P01632 mus musculu
43	365.5	53.7	108	1	KV1H_HUMAN	P01600 homo sapien
44	362.5	53.2	111	1	KV3C_MOUSE	P01656 mus musculu
45	362	53.2	113	1	KV2B_HUMAN	P01615 homo sapien

## ALIGNMENTS

RESULT 1  
KV4C\_HUMAN  
ID KV4C\_HUMAN STANDARD: PRT: 134 AA.

AC P06314;  
DT 01-JAN-1988 (Rel. 06, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-IV region B17 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_Taxid=9606;

RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE-66041854; PubMed-2997713;

RA Marsh P., Mills F., Gould H.;

RT "Detection of a unique human V kappa IV germline gene by a cloned

RT cDNA probe.";

RL Nucleic Acids Res. 13:6531-6544(1985).

RM [2]  
RP REVISION TO 76.

RA Marsh P.;

RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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CC EMBL; X02990; CAA26733.1; -.

DR PIR; A01905; K4H017.

DR HSSP; P01789; IMCP.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR Immunoglobulin V region; Signal.

KW SIGNAL

FT CHAIN 1 20

FT DOMAIN 21 134

FT DOMAIN 44 60

FT DOMAIN 61 75

FT DOMAIN 76 82

FT DOMAIN 83 114

FT DOMAIN 115 121

FT DOMAIN 122 133

FT DISUFID 43 114

FT NON\_TER 134

SQ SEQUENCE 134 AA; 14966 MW; 6413A22PD0738832 CRC64;

Query Match 83.9%; Score 571.5; DB 1; Length 134;  
Best Local Similarity 86.28; Pred. No. 2e-52;

```

Matches      112:   Conservative        6:   Mismatches      11:   Indels       1:   Gaps      1,
OY          4 QAOVLILLIWSGTCGGDVIYLTQSPDSLAVSLGERATITCKSSQSGLNSRRENTLAWYQ 63
Db          4 OQOVGFISLLMLTSGVAGDVIMTQSDPSLAVSLGERATITCKSSQSGLNSRKNYLAWYQ 63
OY          64 OKPGCPPKLLIYWASTRESGVDPFRSGSGSCTDFLTITSSLQAEVAYVAYYCQSNL-YT 122
Db          64 OKPGCPKRLIIYWASTRESGVDPFRSGSGSCTDFLTITSSLQAEVAYVAYYCQYYTNLPWT 123
OY          123 FEGGTGRVEIK 132
Db          124 FEGGTGRVEIK 133

RESULT      2
KY4B_HUMAN
ID           KY4B_HUMAN              STANDARD:             PRT:       133 AA.
AC           P06313;
DT           01-JAN-1988 (Rel. 06, Created)
DD           01-JAN-1988 (Rel. 06, Last sequence update)
DE           15-JUL-1999 (Rel. 38, Last annotation update)
DEF          Ig kappa chain V-Iv region JI precursor.
OS           Homo sapiens (Human).
OC           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN           NCBI_TaxID=9606;
RP           [1]
RX           MEDLINE=86041853; PubMed=2997712;
RA           Klobbeck H.G., Bornkamm G.W., Combiato G., Mocikat R., Pohlenz H.D.,
RT           Zachau H.G.;
RR           "Subgroup IV of human immunoglobulin k light chains is encoded by a
RL           single germline gene.";
RS           Nucleic Acids Res. 13:6515-6529(1985).
CC           -----
CC           This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC           -----
DR           EMBL; Z00022; CAAT7317.1; -.
DR           PIR; A01904; K4HOUT.
DR           HSSE; P01789; IMCP.
DR           InterPro; IPR003006; IG_MHC.
DR           InterPro; IPR003596; IG_V.
DR           Pfam; PF00047; Ig; 1.
DR           SMART; SM00406; IGV; 1.
KW           Immunoglobulin V region; Signal.
FT           SIGNAL                     1..20
FT           CHAIN                      21..133
FT           DOMAIN                     21..43
FT           DOMAIN                     44..60
FT           DOMAIN                     61..75
FT           DOMAIN                     76..82
FT           DOMAIN                     83..114
FT           DOMAIN                     115..122
FT           DOMAIN                     123..132
FT           DISULFID                     43..114
FT           NON_TER                     133
SQ           SEQUENCE                  133 AA; 14652 MW; 5FB3953066744AF4 CRC64;

Query Match      81.1%; Score 552; DB 1; Length 133;
Best Local Similarity 83.7%; Pred. No. 2, le-50;
Matches 108: Conservative 6; Mismatches 15; Indels 0; Gaps 0;
OY          4 QAOVLILLIWSGTCGGDVIYLTQSPDSLAVSLGERATITCKSSQSGLNSRRENTLAWYQ 63
Db          4 OQOVGFISLLMLTSGVAGDVIMTQSDPSLAVSLGERATITCKSSQSGLNSRKNYLAWYQ 63
```

OY	64	QKRGPPKLLIYWASTRESGVDPDRSGSGSDPFLTIISSLOAEVAVYYCQSNTLYTE	123
DB	64	QKRGPPKLLIYWASTRESGVDPDRSGSGSDPFLTIISSLOAEVAVYYCQIDITPTF	123
OY	124	GCGTRVEIK	132
DB	124	GCGTRVEIK	132
<hr/>			
RESULT	3		
KV40_HUMAN			
ID	KV40_HUMAN	STANDARD:	PRT: 121 AA.
AC	P06312:		
DT	01-JAN-1988 (Rel. 06, Created)		
DT	01-JAN-1988 (Rel. 06, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-Iv region precursor (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A!		
RX	MEDLINE=86041853; PubMed=299712;		
RA	Klobeck H.G., Bornkamm G.W., Combrlatto G., Mocikat R., Pohlenz H.D.,		
RA	Zachau H.G.;		
RT	"Subgroup IV of human immunoglobulin K light chains is encoded by a		
RL	single germline gene.";		
RJ	Nucleic Acids Res; 13:6515-6529(1985).		
CC	- I - MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; Z00023; CAN7/318.1; -.		
DR	PIR; A01902; K4H0.		
DR	HSSP; P01789; IMCP.		
DR	InterPro; IPRO03006; IG_MHC.		
DR	InterPro; IPRO03596; IG-V.		
DR	Pfam; PF00047; Ig_1.		
DR	SMART; SM00406; IGV; 1.		
KM	Immunoglobulin V region; Signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	>121
FT	DOMAIN	21	43
FT	DOMAIN	44	60
FT	DOMAIN	61	75
FT	DOMAIN	76	82
FT	DOMAIN	83	114
FT	DOMAIN	115	121
FT	DISULFYD	43	114
FT	NON_TER	121	121
SO	SEQUENCE	121 AA;	13380 MM; 9586AD418BD33974 CRC64;
<hr/>			
Query Match		75.6%; Score 515; DB 1; Length 121;	
Best Local Similarity		85.3%; Pred. No. 1.3e-46;	
Matches	99; Conservative	6; Mismatches 11; Indels	0; Gaps 0;
OY	4	QAQVLILLILWVGRCGDIVLTQSPDSLAVSLGERAATISCKSSQGLNSRRRENTLAYQ	63
DB	4	QIQVETISLLIMISGAYGDIVMTQSPDSLAVSLGERAATINCKSSQSVLVSNKNKTYLAHQ	63
OY	64	QKRGPPKLLIYWASTRESGVDPDRSGSGSDPFLTIISSLOAEVAVYYCQSYN	119
DB	64	QKRGPPKLLIYWASTRESGVDPDRSGSGSDPFLTIISSLOAEVAVYYCQOYS	119

```
RESULT 4
KV3L_HUMAN STANDARD; PRT; 114 AA.
ID KV3L_HUMAN
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hope-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (Aug-1996) to the SWISS-PROT data bank
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSSP; P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 41 FRAMEWORK-2.
FT DOMAIN 4 55 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 62 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 6 94 FRAMEWORK-3.
FT DOMAIN 7 95 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 8 101 FRAMEWORK-4.
FT DISULFID 102 113 BY SIMILARITY.
FT NON_TER 114 114
SO SEQUENCE 114 AA; 12640 MW; 0647F1D17E236485 CRC64;
```

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Query Match 73.8%; Score 502.5; DB 1; Length 114;
Best Local Similarity 86.7%; Pred. No. 2.4e-45;
Matches 98; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

OY 21 DIVLQSPSLAVSLGERTISCKSSQSLNSTRRENYLAWYQKRGQPKLLIYNASTR 80
DB 1 DIVMTQSPDSLAVSLGERATINCKSSQSLVLSNSKNYLAWYQKRGQPKLLIYNASTR 60

OY 81 ESGVDFRSGSGSDFTLTISLQAEADVAVVYCTQSYNLTYPFGQGTVEIK 132
DB 61 ESGVDFRSGSGSDFTLTISLQAEADVAVVYCTQSYSTPSFGQGTVEIK 113

RESULT 5
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RL
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RA Jirik F.R., Sorage J., Fong S., Heitzmann J.G., Curo J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC -----
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CC -----
DR EMBL; M12740; AAA58992.1; -
DR PIR; A01898; K3HUCI.
DR HSSP; P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 22 44 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 23 54 FRAMEWORK-2.
FT DOMAIN 24 69 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 25 70 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 26 77 FRAMEWORK-3.
FT DOMAIN 27 108 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 28 109 FRAMEWORK-4.
FT DOMAIN 29 118 BY SEGMENT.
FT DISULFID 119 129
FT NON_TER 129 129
SO SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;
```

```
Query Match 65.5%; Score 446; DB 1; Length 129;
Best Local Similarity 66.7%; Pred. No. 2e-39;
Matches 90; Conservative 20; Mismatches 15; Indels 10; Gaps 3;

OY 1 MDSQAVLILLVLVSGTGDIVTQSPDSLAVSLGERATISCKSSQSLNSTRRENYLA 60
DB 1 MEAPQQLFLILLMLPPTTGEIYWTQSPATILSVGERATISCAASQSVSN-----LA 54

OY 61 WYQKRGQPKLLIYNASTRSGVDFRSGSGSDFTLTISLQAEADVAVVYCTQSYN 119
DB 55 WYQKRGQPKLLIYNASTRSGVDFRSGSGSDFTLTISLQAEADVAVVYCTQSYN 113

OY 120 --LYTFGQGTVEIK 132
DB 114 WPPWTFGQGTVEIK 128

RESULT 6
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
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QY	51	WYQKPGPDKPLIKLWASRGIDVITFQSPDGLAVSGERATISCKSSQSLNSTRFENYIA	60
DB	55 <td>WYQKRGSGSPRLINDADASSRANGITFDRFSGSGSIDFTLLISRLPEDEFAVYICQOYIS</td> <td>114</td>	WYQKRGSGSPRLINDADASSRANGITFDRFSGSGSIDFTLLISRLPEDEFAVYICQOYIS	114
QY	120	LYTFGQGTKEIK	132
DB	115	PYTFGQGTKEIK	127
RESULT	11		
RV3I_MOUSE			
ID	KV3I_MOUSE	STANDARD:	PRT, 131 AA.
AC	P01661.		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-II region MOPC 63 precursor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE OF 1-35.		
RX	MEDLINE=78235887; PubMed=98179;		
RA	Bursteln Y., Schechter I.;		
RT	"Primary structures of N-terminal extra peptide segments linked to		
RT	the variable and constant regions of immunoglobulin light chain		
RT	precursors: implications on the organization and controlled		
RT	expression of immunoglobulin genes."		
RL	Biochemistry 17:2392-2400(1978).		
RN	[2]		
RP	SEQUENCE OF 21-131.		
RX	MEDLINE=73140225; PubMed=4691517;		
RA	McKean D.J., Potter M., Hood L.E.;		
RT	"Mouse immunoglobulin chains. Pattern of sequence variation among		
RT	kappa chains with limited sequence differences."		
RL	Biochemistry 12:760-771(1973).		
RN	[3]		
RP	REVISTIONS.		
RX	MEDLINE=79012520; PubMed=99744;		
RA	McKean D.J., Bell M., Potter M.;		
RT	"Mechanisms of antibody diversity: multiple genes encode structurally		
RT	related mouse kappa variable regions."		
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).		
DR	PIR: A01935; KVM5M6.		
DR	HSSP; P01789; IMCP.		
DR	InterPro: IPR003306; Ig_MHC.		
DR	InterPro: IPR003596; Ig_V.		
DR	PIfam: PF00047; Ig_1.		
DR	SMART: SM00406; IGV: 1.		
KW	Immunoglobulin V region; Signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	131
FT	DOMAIN	21	43
FT	DOMAIN	44	58
FT	DOMAIN	59	73
FT	DOMAIN	74	80
FT	DOMAIN	81	112
FT	DOMAIN	113	121
FT	DOMAIN	122	131
FT	DISULFID	43	112
FT	NON_TER	131	131
SO	SEQUENCE	131 AA;	D212EC9F08DC880A CRC64;
QY	Query Match	60.0%;	Score 408.5; DB 1; Length 131;
DB	Best Local Similarity	62.4%;	Pred. No. 1.6e-35;
Matches	83; Conservative	21;	Mismatches 26; Indels 3; Gaps 2;
QY	1	MNSQAVLILLWVSGTGTIVITFQSPDGLAVSGERATISCKSSQSLNSTRFENYIA	60
DB	1	METPTPLLVLLWLVGVSGNITVLQSPASLAVSGERATISCKSSQSLNSTRFENYIA	58

QY	61	WYQOKPGPPLKILTYMASTRSGVDFRSGSSGDFLTITSSLOAEVAVYCTQK-SYN	119
Db	59	WYQOKPGPPLKILTYLANLESSEGVARESGSSGRIDFTLTIDPVAEADDAATYYCCQNNED	118
QY	120	LYTEGGGTGKVEIK	132
Db	119	PWTEGGGTGLEIK	131
RESULT	12		
ID	KV3F_MOUSE	STANDARD;	PRT; 132 AA.
AC	P01658;		
DT	21-JUL-1986 (Rel: 01, Created)		
DT	21-JUL-1986 (Rel: 01, Last sequence update)		
DT	15-JUL-1999 (Rel: 36, Last annotation update)		
DE	Ig kappa chain V-II region MOPC 321 precursor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
CX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE OF 1-37.		
RX	MEDLINE=78235887; PubMed=981179;		
RA	Burstein Y., Schechter I.;		
RT	"Primary structures of N-terminal extra peptide segments linked to		
RT	the variable and constant regions of immunoglobulin light chain		
RT	precursors: implications on the organization and controlled		
RT	expression of immunoglobulin genes."		
RL	Biochemistry 17:2392-2400(1978).		
RN	[2]		
RP	SEQUENCE OF 21-132.		
RX	MEDLINE=73140224; PubMed=4120529;		
RA	McKean D.J., Potter M., Hood L.E.;		
RT	"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa		
RT	chain."		
RL	Biochemistry 12:749-759(1973).		
CC	-1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS		
CC	BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT		
CC	REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY		
CC	RESIDUES.		
DR	PIR; A01933; KVS32.		
DR	HSSP; P01607; IREI.		
DR	InterPro: IPR003006; IG_MHC.		
DR	InterPro: IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig_1.		
DR	SMART; SM00406; IgV_1.		
KW	Immunoglobulin V region; Bence-Jones protein; Signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	132
FT	DOMAIN	21	43
FT	DOMAIN	49	58
FT	DOMAIN	55	73
FT	DOMAIN	74	80
FT	DOMAIN	81	112
FT	DOMAIN	113	121
FT	DOMAIN	122	131
FT	DISULFID	43	112
FT	NON_TER	132	132
SQ	SEQUENCE	132 AA;	14523 MW; 9F3B809B873FBE9 CRC64;
Query Match		60.0%;	Score 408.5; DB:1; Length 132;
Best Local Similarity		58.6%;	Pred. No. 1.6e-35;
Matches	78;	Conservative	28; Mismatches 24; Indels 3; Gaps 2;
OY	1	MDSQAVILILLAWSGRCGDIVLQSPDSLAVSGERATICKSSQSLNSRTRENTYA	60
Db	1	METDILLMLVLLWPLWPGSTGDIVLQSPASLAVSGQRTATISCRASKSV--NTYNSNFWZ	58
OY	61	WYQOKPGPPLKILTYMASTRSGVDFRSGSSGDFLTITSSLOAEVAVYCTQK-SYN	119

ID	NAME	STANDARD	PRT	116 AA
Db	59*WVZRPZPGPRLKILIVRASNLGSGIPARRSGSSRFBFLTLIBPVABADVATVFCZSZSB2B			118
Oy	120 LYTPEGCKVLEK			132
Db	119 PWTFGSGTKLEIK			131
RESULT 13				
ID	KV31_HUMAN	STANDARD	PRT	115 AA.
AC	P04433			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-II region V6 precursor (fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85087932; PubMed=6440122;			
RA	Pech M., Zachau H.G.;			
RT	"Immunoglobulin genes of different subgroups are interdigitated			
RT	within the Vκ locus.";			
RL	Nucleic Acids Res. 12:9229-9236(1984).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; X01668; ; NOT_ANNOTATED_CDS.			
DR	PIR; A01900; K3HDVG.			
DR	HSSP; P01789; IMCP.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IgV; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL	1	20	
FT	CHAIN	21	>115	
FT	DOMAIN	21	43	
FT	DOMAIN	44	54	
FT	DOMAIN	55	69	
FT	DOMAIN	70	76	
FT	DOMAIN	77	108	
FT	DOMAIN	109	115	
FT	DISULFID	43	108	
FT	NON_TER	115	115	
SO	SEQUENCE	115 AA;	12575 MM;	2DE47CDA3A1D555 CNC64;
Query Match 58.1%; Score 396; DB 1; Length 115;				
Best Local Similarity 65.5%; Pred. No. 2.7e-34;				
Matches 78; Conservative 17; Mismatches 18; Indels 6; Gaps 1;				
Oy	1 MDSQAQVILLILLWVSGTCGDIVLTQSPDSLAVSLGERATYISCKSSQSLNSRNTRENTIA 60			
Db	1 MEAPAQQLLELLILLPDTTGEIVLQSPATLSISGERATLSCKRASGV-----SYIA 54			
Oy	61 WYQCKPGQPKLLIYMASTRSGVDRSGSGSGGDFLTITSSLDQAEVAVYYCTQSYN 119			
Db	55 WYQCKPGQPKLLIYDASNRATGIPARRSGSGSGDFLTITSSLEPEDEFAVYYCOQREN 113			
RESULT 14				
ID	KV31_HUMAN	STANDARD	PRT	116 AA.
CC	P04434;			

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DN      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region VH precursor (Fragment) .
OS      Homo sapiens (Human) .
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX      NCB1_TaxID=9606;

RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=85087932; PubMed=6440122;
RA      Pech M., Zachau H.G.;
RT      "Immunoglobulin genes of different subgroups are interdigitated
RL      within the VK locus."
RL      Nucleic Acids Res. 12:9229-9236(1984) .
CC      -----
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CC      or send an email to license@isb-sib.ch) .
CC      -----
DR      EMBL; X02725; -; NOT_ANNOTATED_CDS.
DR      PIR; A01901; K3HUVH.
DR      HSSP; A01789; ZMCP.
DR      InterPro; IPR003006; I9_MHC.
DR      InterPro; IPR003596; I9_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SMO0406; Igv; 1.
KW      Immunoglobulin V region; Signal.
FT      SIGNAL
FT      CHAIN
FT      DOMAIN
FT      DOMAIN
FT      DOMAIN
FT      DOMAIN
FT      DOMAIN
FT      DOMAIN
FT      DISULFID
FT      NON_TER
SQ      SEQUENCE

1      20      IG KAPPA CHAIN V-II REGION VH.
21      >116      FRAMEWORK-1.
22      43      COMPLEMENTARITY-DETERMINING-1.
23      55      FRAMEWORK-2.
24      70      COMPLEMENTARITY-DETERMINING-2.
25      77      FRAMEWORK-3.
26      109      COMPLEMENTARITY-DETERMINING-3.
27      110      BY SIMILARITY.
28      109
29      116
30      116      12757 MW; 51CD5BA53B21929 CMC64;

Query Match      57.9%; Score 394.5; DB 1; Length 116;
Best Local Similarity      64.2%; Pred. No. 3,9e-34;
Matches      77; Conservative      18; Mismatches      20; Indels      5; Gaps      1;

OY      1      MDSQAQVILILLVWSGTFCGDIVLTQSPDLSAVSLGERATTSCKSSQSLNSRRENTYLA      60
      :::::|||||:      ::::|||||:|:::|||||:|||||:|
DB      1      MEAPQALLFLILLMDPTREITVIMQSPPTLSLSPGERVTLSCRASQSVSSS-----YLT      55

OY      61      WYQQKPGQPKRLIYMASTRGSGVDVRSGSSGSGFDPLTITSSLDQAEDEVAYYYCQSTNLT      120
      ||| ||||| |::| ||||| ||| :| ||| ||||| ||||| || ||||| |::|
DB      56      WYQQKPGQAPRLIYGASTRATSIIPARESGSGSGFDPLTITSSLDQAEDEVAYYYCQSDHNL      115

RESULT      15
KV3P_MOUSE      STANDARD;      PRT;      110 AA.
AC      P01668;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region PC 7210.
OS      Mus musculus (Mouse) .
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX      NCB1_TaxID=10090;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=79073152; PubMed=103003;

```

RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity";  
 RT Nature 276:785-790(1978).  
 RL PIR: D01937; KWS10.

DR HSSP: P01789; IMCP.  
 DR InterPro: IPR003006; I9\_MHC.  
 DR InterPro: IPR003596; I9\_V.  
 DR Pfam: PF00047; I9: 1.  
 DR SMART: SM00406; IGV: 1.  
 KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 39 53 FRAMEWORK-2.  
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 61 92 FRAMEWORK-3.  
 FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 101 110 FRAMEWORK-4.  
 FT DISULFID 23 92 BY SIMILARITY.  
 FT NON\_TER 110 110  
 SQ SEQUENCE 110 AA: 11950 MW: 69F1A5CE886B1249 CRC64;

Query Match 57.9%; Score 394; DB 1; Length 110;  
 Best Local Similarity 70.5%; Pred. No. 4, 1e-34;  
 Matches 79; Conservative 11; Mismatches 20; Indels 2; Gaps 1;

OY 21 DIVLTQSPDLSAVSLGERATISCKSSQSLNSRTRENYLAWYQKPGPKLITYWASTR 80  
 DB 1 DIVLTQSPDLSAVSLGQRATISCKASQSL--DYDGDSYNMWYQKPGPKLITYASNL 58  
 OY 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYNLYTGGGTKEIK 132  
 DB 59 ESGIPARFSGSGSGTDFTLNHPVEEDATATYCHQSEDDPWTEGSGTKLEIK 110

Search completed: August 26, 2002, 15:05:39  
 Job time: 358 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: August 26, 2002, 15:05:03 ; Search time 36.13 Seconds

(without alignments)  
632.032 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681  
Sequence: 1 MDSQAQVLLILLMWSTGCG.....YCTQSYNLYFGGQTKVEIK 132

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :

1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*  
15: SP virus: \*  
16: SP bacteriophage: \*  
17: SP archaea: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	410.5	60.3	107	11 Q9ER29	Q9ER29 mus musculus
2	400	58.7	238	11 Q99M37	Q99M37 mus musculus
3	388	57.0	107	4 Q96SA9	Q96SA9 homo sapien
4	384	56.4	107	4 Q9UL81	Q9UL81 homo sapien
5	383.5	56.3	111	11 Q920E9	Q920E9 mus musculus
6	379.5	55.7	108	4 Q9UL77	Q9UL77 homo sapien
7	379	55.1	109	4 Q9UL79	Q9UL79 homo sapien
8	375.5	54.8	108	4 Q9UL78	Q9UL78 homo sapien
9	373.5	54.7	108	4 Q9UL83	Q9UL83 homo sapien
10	368	54.0	109	4 Q9UL86	Q9UL86 homo sapien
11	368	54.0	109	4 Q9UL85	Q9UL85 homo sapien
12	352.5	51.8	114	4 Q9UL80	Q9UL80 mus musculus
13	348.5	51.2	234	11 Q91WF8	Q91WF8 mus musculus
14	341	50.1	104	11 Q91L82	Q91L82 mus musculus
15	341	50.1	104	11 Q91L82	Q91L82 mus musculus
16	339.5	49.9	233	11 Q91WS9	Q91WS9 mus musculus

17	336.5	49.4	99	11 Q91L74	Q91L74 mus musculus
18	331.5	48.7	214	11 Q91L85	Q91L85 mus musculus
19	324.5	47.7	103	11 Q91L80	Q91L80 mus musculus
20	319.5	46.9	116	4 Q96PF6	Q96PF6 homo sapien
21	319	46.8	130	4 Q9NP29	Q9NP29 homo sapien
22	315.5	46.3	298	11 Q9QXF0	Q9QXF0 mus musculus
23	315	46.3	225	11 Q91W12	Q91W12 mus musculus
24	308.5	45.3	109	11 Q920E6	Q920E6 mus musculus
25	307.5	45.2	127	11 Q925S9	Q925S9 mus musculus
26	303.5	44.6	101	11 Q91L78	Q91L78 mus musculus
27	303.5	44.6	109	6 Q9N0W5	Q9N0W5 oryctolagus
28	300	44.1	241	11 Q921A6	Q921A6 mus musculus
29	296.5	43.5	107	11 Q91L84	Q91L84 mus musculus
30	292	42.9	106	5 Q90410	Q90410 schistosoma
31	286.5	42.1	211	11 Q91XL0	Q91XL0 mus musculus
32	280.5	41.2	97	11 Q91L76	Q91L76 mus musculus
33	257.5	37.8	218	11 Q925S1	Q925S1 mus musculus
34	243	35.7	107	4 Q9NSD6	Q9NSD6 homo sapien
35	242.5	35.6	226	4 Q96E61	Q96E61 homo sapien
36	240.5	35.3	108	4 Q96S80	Q96S80 homo sapien
37	238	34.9	235	11 Q99M11	Q99M11 mus musculus
38	233.5	34.3	107	4 Q9UL82	Q9UL82 homo sapien
39	226.5	33.3	112	4 Q96JD1	Q96JD1 homo sapien
40	217	31.9	116	4 Q96JD0	Q96JD0 homo sapien
41	215	31.6	112	4 Q96JD2	Q96JD2 homo sapien
42	207	30.4	233	11 Q91V32	Q91V32 m adult mal
43	192.5	28.3	233	4 Q96I69	Q96I69 homo sapien
44	191	28.0	109	11 Q9ET13	Q9ET13 mus musculus
45	178	26.1	154	11 Q91XK2	Q91XK2 mus musculus

## ALIGNMENTS

RESULT 1  
Q9ER29 ID Q9ER29 PRELIMINARY; PRT; 107 AA.  
AC Q9ER29;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;  
RT "Cloning and sequencing of the light chain fragment of variable region  
RT genes of an anti-hTNF-a monoclonal antibody.";  
RL J. Cell. Mol. Immunol. 12:21-26(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RT "Construction and sequencing of the single-chain antibody gene of a  
RT human TNF-alpha specific monoclonal antibody.";  
RL T1 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF62753; AAG23804.1; -  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR003599; Iq.  
DR InterPro; IPR003006; Iq.  
DR InterPro; IPR003596; IqLV.  
DR Pfam; PF00047; Iq; 1.  
DR SMART; SM00409; Iq; 1.  
DR SMART; SM00406; Iq; 1.  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11784 MW; 2B15E6A6604A26C3 CRC64;



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OY 81 ESGVDPDRFSGSGGTDFTLTISLSLAQADVAVYCTOSYNLTFFGOGTKEIK 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 55 QSGVPRFSGSGGTDFTLTISLSLAQADVAVYCTOSYNLTFFGOGTKEIK 106

RESULT 5
O920E9 PRELIMINARY: PRT; 111 AA.
AC O920E9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PTERIN-MIMICKING ANTI-IDIOLOPE KARPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ackin J.D., Jape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.";
RT Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF307935; AAL09419.1; -.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA658526 CRC64;

Query Match
Best Local Similarity 56.3%; Score 383.5; DB 11; Length 111;
Matches 79; Conservative 11; Mismatches 20; Indels 3; Gaps 2;

OY 21 DIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLAWYQKPGPKLLIYNASTR 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIVLTQSPDSLAVSLGERATISCKRAKSV--STSGSYMHWTQKQKPGPKLLIYASNL 58

OY 81 ESGVDPDRFSGSGGTDFTLTISLSLAQADVAVYCTOSYNLTFFGOGTKEIK 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 59 ESGVPRFSGSGGTDFTLTISLSLAQADVAVYCTOSYNLTFFGOGTKEIK 111

RESULT 6
O9UL77 PRELIMINARY: PRT; 108 AA.
AC O9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AAD56273.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
```

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Query Match
Best Local Similarity 55.7%; Score 379.5; DB 4; Length 108;
Matches 75; Conservative 15; Mismatches 16; Indels 7; Gaps 2;

OY 21 DIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLAWYQKPGPKLLIYNASTR 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIVLTQSPDSLAVSLGERATISCKASQSI-----SSYLMWYQKPGKAPNLLIYASSL 54

OY 81 ESGVDPDRFSGSGGTDFTLTISLSLAQADVAVYCTOSYNLTFFGOGTKEIK 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 55 QSGVPRFSGSGGTDFTLTISLSLAQADVAVYCTOSYNLTFFGOGTKEIK 107

RESULT 7
O9UL78 PRELIMINARY: PRT; 109 AA.
AC O9UL78;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -.
DR HSSP: P80362; IWTI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match
Best Local Similarity 55.7%; Score 379; DB 4; Length 109;
Matches 77; Conservative 15; Mismatches 15; Indels 6; Gaps 2;

OY 21 DIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLAWYQKPGPKLLIYNASTR 80
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIVLTQSPDSLAVSLGERATISCKASQSVSS-----YLAWYQKPGKAPNLLIYASSR 55

OY 81 ESGVDPDRFSGSGGTDFTLTISLSLAQADVAVYCTO-SYNLTFFGOGTKEIK 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 56 ATGIDPRFSGSGGTDFTLTISLSLAQADVAVYCTO-SYNLTFFGOGTKEIK 108

RESULT 8
O9UL79 PRELIMINARY: PRT; 108 AA.
AC O9UL79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035035; AAD56271.1; -.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003596; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5645F19724FB4E CRC64;

Query Match 55.1%; Score 375.5; DB 4; Length 108;
Best Local Similarity 67.3%; Pred. No. 1.9e-32;
Matches 76; Conservative 11; Mismatches 19; Indels 7; Gaps 2;

QY 21 DIVLTGSPDSLAVSLGSRATISCKSSOSLNSRTRENYLAWYQKPGQPKLLIYMASTR 80
DB 1 DIVMTGSPDSLAVSLGSRATISCKSSOSLNSRTRENYLAWYQKPGQPKLLIYMASTR 54
QY 81 ESGVPRFSGSGSGTDEFTLTITSSLAQEDVAVYYCTOSYNL-YTFGGGTVEIK 132
DB 55 QSGVPRFSGSGSGTDEFTLTITSSLAQEDFAVYYCCOYTSPPFTFGGTVEIK 107

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC 09UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003596; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 54.8%; Score 373.5; DB 4; Length 108;
Best Local Similarity 67.5%; Pred. No. 3e-32;
Matches 77; Conservative 11; Mismatches 17; Indels 9; Gaps 3;

QY 21 DIVLTGSPDSLAVSLGSRATISCKSSOSLNSRTRENYLAWYQKPGQPKLLIYMASTR 80
DB 1 DIVMTGSPDSLAVSLGSRATISCKSSOSLNSRTRENYLAWYQKPGQPKLLIYMASTR 54
QY 81 ESGVPRFSGSGSGTDEFTLTITSSLAQEDVAVYYCTOSYNL-YTFGGGTVEIK 132
DB 55 QSGVPRFSGSGSGTDEFTLTITSSLAQEDVAVYYCTOSYNL-YTFGGGTVEIK 132
```

```

DB 55 QSGVPRFSGSGSGTDEFTLTITSSLAQEDVAVYYC-QKYNAPRFGGTVEIK 107
:|||||
RESULT 10
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC 09UL83;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035031; AAD56267.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003596; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 54.7%; Score 372.5; DB 4; Length 108;
Best Local Similarity 67.5%; Pred. No. 3.9e-32;
Matches 77; Conservative 16; Mismatches 12; Indels 9; Gaps 3;

QY 21 DIVLTGSPDSLAVSLGSRATISCKSSOSLNSRTRENYLAWYQKPGQPKLLIYMASTR 80
DB 1 DIVMTGSPDSLAVSLGSRATISCKSSOSVSSN-----LAWYQKPGQPKLLIYMASTR 54
QY 81 ESGVPRFSGSGSGTDEFTLTITSSLAQEDVAVYYCTOSYNL-YTFGGGTVEIK 132
DB 55 ATGIPARFSGSGSGTDEFTLTITSSLAQEDFAVYYC-QHYNNMPTFGGTVEIK 107

RESULT 11
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC 09UL86;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035028; AAD56264.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003596; Ig_MHC.
```







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 14:58:51 ; Search time 42.03 Seconds

(without alignments)  
348,840 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681

Sequence: 1 MDSSAQVLLILLMLWVGTCG.....YCTSYNLYTFGCTKWEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	681	100.0	132	21	AA07966
2	629	92.4	132	21	AA07964
3	596	87.5	148	10	AA093078
4	592	86.9	239	16	AA076087
5	580.5	85.2	137	18	AA010545
6	575.5	84.3	137	18	AA010544
7	567.5	83.3	137	21	AA095243
8	559.5	82.2	133	15	AA059509
9	557.5	81.9	133	9	AA080894
10	557	81.8	134	18	AA06206
11	555.5	81.6	240	22	AA000815

12	555	81.5	141	20	AA24374	Human monoclonal a
13	553.5	81.3	135	21	AA03714	Immunoglobulin Kap
14	548	80.5	241	13	AA028809	Vector pMDR1007.
15	547.5	80.4	240	20	AA050161	Human reshaped F19
16	544.5	80.0	133	17	AA085909	Monoclonal antibod
17	544.5	80.0	134	20	AA050690	Human Hum4 VL Clat
18	539.5	79.2	133	15	AA048633	Human Hum4 VL Clat
19	539.5	79.2	134	14	AA030485	V kappa region of
20	538.5	79.1	137	17	AA010547	Wild type murine a
21	538.5	79.1	139	18	AA099469	Monoclonal antibod
22	534.5	78.5	137	18	AA021655	Chimeric Mab 15 PC
23	531.5	78.0	128	21	AA056734	Amino acid sequenc
24	531.5	78.0	134	13	AA025158	V-region of L-chain
25	530.5	77.9	137	18	AA021653	Mouse Mab 15 Light
26	528.5	77.6	133	21	AA090719	CC49 VL region pro
27	528.5	77.6	133	21	AA057051	Amino acid sequenc
28	528.5	77.6	133	22	AA002138	Mouse partial anti
29	528.5	77.6	134	14	AA083117	Sequence encoded b
30	525.5	77.2	133	20	AA050154	Murine monoclonal
31	525.5	77.2	240	20	AA050156	Chimeric mouse/hum
32	524.5	77.0	244	21	AA096305	Human IGFAM-17 Imm
33	522.5	76.7	134	22	AA074792	Anti-CA125 bifunct
34	519.5	76.3	154	21	AA053686	Human colon cancer
35	513.5	75.4	495	18	AA032480	Growth factor CATR
36	513.5	75.4	495	20	AA06908	CATR-REV aminoac
37	507.5	74.5	113	20	AA065565	Amino acid sequenc
38	504.5	74.1	113	22	AA050145	Antibody F19 human
39	503	73.9	113	22	AA062769	Human HIV-1 monoc
40	502.5	73.8	155	18	AA032483	Kappa light chain
41	502.5	73.8	155	20	AA06912	Human variable kap
42	502.5	73.8	342	18	AA032482	Growth factor TLHL
43	502.5	73.8	342	20	AA06909	TLHL amino acid se
44	500.5	73.5	113	20	AA050143	Antibody F19 human
45	498.5	73.2	113	15	AA050314	Humanised light ch

## ALIGNMENTS

RESULT	1	
AA07966	ID	AA07966 standard; Protein; 132 AA.
XX	AA07966;	
AC	14-NOV-2000	(first entry)
XX		
DE	A light chain variable region of humanised 3S1 antibody.	
XX		
XX	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;	
KW	Autoimmune disease; infectious disease; inflammatory disorder;	
KW	systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;	
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;	
KW	multiple sclerosis; transplant rejection; proliferative disease;	
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;	
KW	aplastic anaemia; myeloid dysplasia syndrome.	
XX		
OS	Synthetic.	
OS	Mus sp.	
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
FT	Peptide	1..20
FT	Protein	/note="signal peptide"
FT		21..132
FT		/note="mature protein"
FT	Region	44..60
FT		/note="complementarity determining region 1"
FT	Region	76..82
FT		/note="complementarity determining region 2"
FT	Region	115..122
FT		/note="complementarity determining region 3"
XX		

```

PN WO200047625-A2.
XX
XX 17-AUG-2000.
XX
XX 09-FEB-2000; 2000WO-US03303.
XX
XX 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
XX (GEMV ) GENETICS INST INC.
XX
XX Co MS, Vasquez M, Carreno B, Celinker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
XX WPI; 2000-524532/47.
DR N-PSDB; AAA59695.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases -
XX
XX Example 3; Fig 2B; 162pp; English.
XX
XX The present sequence represents the light chain variable region of the
CC humanised murine antibody 3D1. The antibody has a binding specificity to
CC B7 molecules. The antibody is used to construct humanized
CC immunoglobulins, which comprise an antigen binding region of non-human
CC origin and a portion of a human immunoglobulin. The humanized
CC immunoglobulins are useful for treating autoimmune diseases, infectious
CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
XX Sequence 132 AA:
SQ
Query Match 100.0%; Score 681; DB 21; Length 132;
Best Local Similarity 100.0%; Pred. No. 6.7e-47;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSOAOVLILLILWVGTCGDIYLTQSPDSLAVSLGRATISCKSSOSILNSTRRENYLA 60
Db 1 mdsqagvllllllwvsgtcgdvltqspdslavslgratiscskssqslinstrrenyla 60
QY 61 WYQOKPGQPKLLIYWASTRESGVNPRFSGSGSGTFTLTITSSIAQEDVAVVYCTQSYNL 120
Db 61 WYQKPGQPKLLIYWASTRESGVNPRFSGSGSGTFTLTITSSIAQEDVAVVYCTQSYNL 120
QY 121 YTFGQGTKEIK 132
Db 121 ytfgggtkveik 132

```

## RESULT 2

```

AAB07964
ID AAB07964 standard; Protein; 132 AA.
XX
AC AAB07964;
XX
DT 14-NOV-2000 (first entry)
XX
DE Amino acid sequence of light chain variable region of 3S1 antibody.
XX
XX Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KM autoimmune disease; infectious disease; inflammatory disorder;
KM systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
KM arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;

```

```

KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH Peptide 1..20
FT /note= "signal peptide"
FT Protein 21..132
FT /note= "mature protein"
FT Region 44..60
FT /note= "complementarity determining region 1"
FT Region 76..82
FT /note= "complementarity determining region 2"
FT Region 115..122
FT /note= "complementarity determining region 3"
XX
XX WO200047625-A2.
XX
XX 17-AUG-2000.
XX
XX 09-FEB-2000; 2000WO-US03303.
XX
XX 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
XX (GEMV ) GENETICS INST INC.
XX
XX Co MS, Vasquez M, Carreno B, Celinker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
XX WPI; 2000-524532/47.
DR N-PSDB; AAA59693.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases -
XX
XX Example 1; Fig 1B; 162pp; English.
XX
XX The present sequence represents the light chain variable region of the
CC murine antibody 3D1. The antibody has a binding specificity to B7
CC molecules. The antibody is used to construct humanized immunoglobulins,
CC which comprise an antigen binding region of non-human origin and a
CC portion of a human immunoglobulin. The humanized immunoglobulins are
CC useful for treating autoimmune diseases, infectious diseases,
CC inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
XX Sequence 132 AA:
SQ
Query Match 92.4%; Score 629; DB 21; Length 132;
Best Local Similarity 90.9%; Pred. No. 8.8e-43;
Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
QY 1 MDSOAOVLILLILWVGTCGDIYLTQSPDSLAVSLGRATISCKSSOSILNSTRRENYLA 60
Db 1 mdsqagvllllllwvsgtcgdvltqspdslavslgratiscskssqslinstrrenyla 60
QY 61 WYQOKPGQPKLLIYWASTRESGVNPRFSGSGSGTFTLTITSSIAQEDVAVVYCTQSYNL 120
Db 61 WYQKPGQPKLLIYWASTRESGVNPRFSGSGSGTFTLTITSSIAQEDVAVVYCTQSYNL 120
QY 121 YTFGQGTKEIK 132

```

|||||  
121 ytfgggtkleik 132

## RESULT 3

AAP93078  
ID AAP93078 standard; peptide; 148 AA.  
XX  
AC AAP93078;  
XX  
AC 14-MAR-1990 (first entry)  
XX  
DE Light chain of monoclonal antibody 6A4.  
XX  
KW Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.  
XX  
PN EP338395-A.  
XX  
PD 25-OCT-1989.  
XX  
PF 12-APR-1989; 89EP-0106463.  
XX  
PR 19-APR-1988; 88DE-3813023.  
XX  
PA (BEHM ) BEHRINGERKE.  
XX  
PI Domdey H, Marget M, von Specht BU;  
XX  
DR WPI: 1989-310861/43.  
XX  
N-PSDB; AAN91663.  
XX  
PT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for  
XX  
PS variable antibody regions.  
XX  
PS Claim 1; page 6; 7pp; german.  
XX  
CC The peptide is encoded by the light chain of monoclonal antibody 6A4.  
CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of  
CC P.aeruginosa. It is used for therapy and diagnosis of infection, and as  
CC a carrier for drugs. The antibody is IgG2a subclass.  
XX  
SQ Sequence 148 AA;

Query Match 87.5%; Score 596; DB 10; Length 148;

Best Local Similarity 86.4%; Pred. No. 4.1e-40;  
Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDSQAQVLLILLWVGTCGDIYLTQSPDSLAVSLGERATISCKSSQSLSNSTRENYLA 60  
|||||  
DB 1 mdsqagvllllllwvsgtcgdiymsgpspslavsaqekvmcsksqslinslrknfla 60  
QY 61 WYQOKRGPQPKLLIYNASTRSGVPPDRFSGSGSGTDFTLTISSLOAEDVAVVYCTQSYNL 120  
|||||  
DB 61 wyqqrpgqspklllywasrtsgvppdrftgsgsgtdftltissvgaedlavvyckqsyyl 120  
QY 121 YTFGGGTKEIK 132  
|||  
DB 121 rtfgggtkleik 132

## RESULT 4

AAR76087  
ID AAR76087 standard; Protein; 239 AA.  
XX  
AC AAR76087;  
XX  
AC 21-NOV-1995 (first entry)  
XX  
DE Mab 55.1 light chain.  
XX  
KW Antigen binding structure; complementarity determining region; CDR;  
KW CA5.1; colorectal cancer; tumor-associated antigen; hybridoma;

KW monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;  
KW transgenic animal; transgenic plant; antibody engineering;  
KW humanized antibody; immunotoxin.

OS Mus sp.

XX  
FH Key Location/Qualifiers  
XX  
FH Peptide 1..20  
FT /label= sig\_peptide  
FT 21..239  
FT Protein /label= Mat.protein  
FT /note= "claim 3, page 98"

WO9515382-A.

08-JUN-1995.

29-NOV-1994; 94WO-GB02610.

03-JUN-1994; 94GB-0011089.

03-DEC-1993; 93GB-0024819.

(ZENE ) ZENECA LTD.

XX Blakely DC, Boot C, Copley CG, Hall SM, Paterson DS;

PI Rose MS, Wright AF;

DR WPI: 1995-215262/28.

N-PSDB; AAQ94036.

PT Antigen binding structures containing CDRs recognising the CA5.1

PS disclosure; Fig.16; 121pp; English.

XX Mab 55.1 (ECACC 93081901) recognises the colorectal tumor-associated

CC antigen CA5.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)

CC chains of CA5.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or

CC v-min humanized 55.1 constructs have been expressed in myeloma

XX cells and E. coli.

XX Sequence 239 AA;

QY 1 MDSQAQVLLILLWVGTCGDIYLTQSPDSLAVSLGERATISCKSSQSLSNSTRENYLA 60

|||||  
DB 1 mdsqagvllllllwvsgtcgdiymsgpspslavsaqekvmcsksqslinslrknfla 60

QY 61 WYQOKRGPQPKLLIYNASTRSGVPPDRFSGSGSGTDFTLTISSLOAEDVAVVYCTQSYNL 120

|||||  
DB 61 wyqqrpgqspklllywasrtsgvppdrftgsgsgtdftltissvgaedlavvyckqsyyl 120

QY 121 YTFGGGTKEIK 132

|||  
DB 121 rtfgggtkleik 132

## RESULT 5

AAW10545  
ID AAW10545 standard; Protein; 137 AA.  
XX  
AC AAW10545;  
XX  
AC 25-SEP-1997 (first entry)  
XX  
DE Humanised murine anti-E-selectin antibody Cy1788V(LB).  
XX  
KW Humanised; murine; mouse; E-selectin; antibody; light chain;

KM variable region; detection; inhibition; mediation; cell adhesion;  
KM diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;  
KM acute respiratory distress syndrome; gross cystic breast disease;  
KM cancer; treatment; splanchic occlusion shock; psoriasis;  
KM complement; chimeric.  
XX  
OS Chimeric - Mus spp.  
OS Chimeric - Homo sapiens.  
OS Synthetic.  
XX  
PN WO9640942-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US09204.  
XX  
PR 07-JUN-1995; 95US-0482112.  
XX  
PA (CYTE-) CYTEL CORP.  
XX  
PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;  
PI Jones S;  
XX  
PI WPI: 1997-077272/07.  
DR N-PSDB: AAT60730.  
XX  
XX Humanised anti-E-selectin antibody - useful for diagnosis and  
PT treatment of, e.g. inflammatory responses, septic shock, acute  
PT respiratory distress syndrome or cancer  
XX  
XX Claim 18; Page 71; 89pp; English.  
XX  
XX The present sequence is the humanised murine anti-E-selectin  
CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can  
CC be used to detect E-selectin, or inhibit E-selectin mediated cell  
CC adhesion. It can also be used to diagnose, reduce or inhibit an  
CC inflammatory response, or the severity of pathologies, e.g. septic  
CC shock, acute respiratory distress syndrome, wound associated  
CC sepsis, acute respiratory distress syndrome or cancer, or treat, e.g.  
CC splanchic occlusion shock, or psoriasis. It can be administered to  
CC a human without inducing an immune response, in addition, the  
CC effector portion of the Ab can interact with various components of  
CC the human immune system, including complement.  
CC  
XX  
SQ Sequence 137 AA;  
  
Query Match 85.2%; Score 580.5; DB 18; Length 137;  
Best Local Similarity 85.0%; Pred. No. 6.4e-39;  
Matches 113; Conservative 8; Mismatches 11; Indels 1; Gaps 1;  
  
QY 1 MDSQAQVLLILLWVGTCGDIVLTQSPDSLAVSLGERATISCKSSOSILNSTRENYLA 60  
Db 5 mesqfivmsllfwsqcgdlwmtqpsdlavslgeratlnckssqslhsqngknylt 64  
QY 61 WYQQRKGPQPKLLIYASTRESGVPRFSGSGSGTFTLTISLSQAEDVAVYVCTQSYNL 120  
Db 65 WYQQRKGPQPKLLIYASTRESGVPRFSGSGSGTFTLTISLSQAEDVAVYVCTQSYNL 124  
QY 121 -YTFGGGTVEIK 132  
Db 125 pltfqggtkveik 137  
  
RESULT 6  
AAW10544  
ID AAW10544 standard; Protein; 137 AA.  
AC AAW10544;  
XX  
DT 25-SEP-1997 (first entry)  
XX  
DE Humanised murine anti-E-selectin antibody CY1788V(LA).

XX  
KM Humanised; murine; mouse; E-selectin; antibody; light chain;  
KM variable region; detection; inhibition; mediation; cell adhesion;  
KM diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;  
KM acute respiratory distress syndrome; gross cystic breast disease;  
KM cancer; treatment; splanchic occlusion shock; psoriasis;  
KM complement; chimeric.  
XX  
OS Chimeric - Mus spp.  
OS Chimeric - Homo sapiens.  
OS Synthetic.  
XX  
PN WO9640942-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US09204.  
XX  
PR 07-JUN-1995; 95US-0482112.  
XX  
PA (CYTE-) CYTEL CORP.  
XX  
PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;  
PI Jones S;  
XX  
PI WPI: 1997-077272/07.  
DR N-PSDB: AAT60729.  
XX  
XX Humanised anti-E-selectin antibody - useful for diagnosis and  
PT treatment of, e.g. inflammatory responses, septic shock, acute  
PT respiratory distress syndrome or cancer  
XX  
XX Claim 17; Page 69; 89pp; English.  
XX  
XX The present sequence is the humanised murine anti-E-selectin  
CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can  
CC be used to detect E-selectin, or inhibit E-selectin mediated cell  
CC adhesion. It can also be used to diagnose, reduce or inhibit an  
CC inflammatory response, or the severity of pathologies, e.g. septic  
CC shock, acute respiratory distress syndrome, wound associated  
CC sepsis, acute respiratory distress syndrome or cancer, or treat, e.g.  
CC splanchic occlusion shock, or psoriasis. It can be administered to  
CC a human without inducing an immune response, in addition, the  
CC effector portion of the Ab can interact with various components of  
CC the human immune system, including complement.  
CC  
XX  
SQ Sequence 137 AA;  
  
Query Match 84.5%; Score 575.5; DB 18; Length 137;  
Best Local Similarity 84.2%; Pred. No. 1.6e-38;  
Matches 112; Conservative 8; Mismatches 12; Indels 1; Gaps 1;  
  
QY 1 MDSQAQVLLILLWVGTCGDIVLTQSPDSLAVSLGERATISCKSSOSILNSTRENYLA 60  
Db 5 mesqfivmsllfwsqcgdlwmtqpsdlavslgeratlnckssqslhsqngknylt 64  
QY 61 WYQQRKGPQPKLLIYASTRESGVPRFSGSGSGTFTLTISLSQAEDVAVYVCTQSYNL 120  
Db 65 WYQQRKGPQPKLLIYASTRESGVPRFSGSGSGTFTLTISLSQAEDVAVYVCTQSYNL 124  
QY 121 -YTFGGGTVEIK 132  
Db 125 pltfqggtkveik 137  
  
RESULT 7  
AAW95243  
ID AAW95243 standard; Protein; 137 AA.  
AC AAW95243;  
XX  
DT 29-AUG-2000 (first entry)  
XX

DE Humanised antibody HuCC49 light chain variable region.  
XX  
XX Humanised antibody; monoclonal antibody; CC49; HuCC49; CDR;  
KW Complementarity determining region; mouse; human; carcinoma;  
KW colon cancer; tumor associated glycoprotein-72; TAG-72;  
KW tumour marker; diagnosis; therapy.  
XX  
OS Chimeric - Mus musculus.  
OS Chimeric - Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 44..59  
FT Region /note= "CDR1"  
FT Region 76..82  
FT Region /note= "CDR2"  
FT Region 115..123  
FT Region /note= "CDR3"  
XX  
XX WO200026394-A1.  
PD 11-MAY-2000.  
XX  
XX 29-OCT-1999; 99WO-US25552.  
XX  
XX 31-OCT-1998; 98US-0106534.  
PR 02-NOV-1998; 98US-0106757.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX  
XX Kashmiri SVS, Padlan EA, Schlom J;  
PI WPI; 2000-365637/31.  
XX  
XX Chimeric variants of CC49 monoclonal antibodies useful for detecting  
PT and treating cancers associated with the expression of the pancreatic  
PT tumor-associated antigen TAG-72 -  
XX  
XX  
XX Disclosure: Fig 4; 76pp: English.  
XX  
XX The present sequence is that of the light chain variable region  
CC (V) of huCC49, a humanised monoclonal antibody (Mab) formed by  
CC grafting hypervariable regions from murine Mab CC49 into VL and VH  
CC frameworks of human Mabs LBN and 21/28' CL, respectively, while  
CC retaining murine framework residues required for integrity of the  
CC antigen combining site structure. HuCC49 binds to the human  
CC pancreatic carcinoma tumor associated glycoprotein-72 (TAG-72), which is  
CC found on the surface of certain human tumours. The invention is  
CC directed towards mouse-human chimeric variants of CC49 Mabs with  
CC minimal murine content, to methods of making such variants, and  
CC their therapeutic application. The invention provides  
CC complementarity determining region (CDR) variants of huCC49 in  
CC which fewer than all 6 CDRs of CC49 are present, and specificity  
CC determining region (SDR) variants of huCC49 in which only SDRs of  
CC at least 1 CDR from CC49 are present. Particular variants of HuCC9  
CC have either L-CDR1 and/or L-CDR2 from human Mab LBN. These  
CC variants have the same or 2-fold lower affinity constant than  
CC HuCC49. Other variants additionally have corresponding human  
CC residues at position 97 of L-CDR3, and positions 60, 61, 62 and 64  
CC of H-CDR2. The variants are used in claimed methods of treating  
CC cancer and for detecting cancer cells that express TAG-72.  
XX  
XX Sequence 137 AA;

Query Match	83.3%	Score	567.5	DB	21	Length	137
Best Local Similarity	82.7%	Pred	No	6.8e-38			
Matches	110	Conservative	11	Mismatches	11	Indels	1
				Gaps	1		
QY	1	MDSQAVLILLILMWSGTCGDIIVLQSPDPLAVSJAERATITCKSSQSILNSRTRENTYA	60				
Db	1	mdsgavqlmllllwsgtcgdlvmsqspdsplavsjgervltnckssqsllysgndknlla	60				

```

Oy      61  WYOOKPGCPKLLIYMASTRSGVPPDRSGSGSTDETLTISLSIQADVAVYCTOSYNL 120
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61  WYQKPGSPKLLIYMASARESGVPDRISGSGSTDFLTLSVQAQDAVYVCQGYSY 120
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

Oy      121  -YTRSGQKTVK 132
        ||  ||  ||  ||  ||
Db      121  PLTFAAGKLEIK 133

```

RESULT	8
AAR59509	
ID	AAR59509 standard; Protein; 133 AA

AC AAR59509;

DT 31-DEC-1994 (first entry)

DE Sequence of the light chain variable region of the mouse NA-8 antibody, including the signal sequence and mature chain.

KW Antibody NA-8; human CD18; complementarity determining region; CDR;

OS Mus musculus.

Key	Location/Qualifiers
FH	21..133
FT	
FT	Mature light chain

PN W09412214-A.

PD 09-JUN-1994.

PF 30-NOV-1993; 93WO-US11611.

PR 01-DEC-1992; 92US-0983949.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Co MS, Landolfi NF;

DR WPI; 1994-199973/24.

[illegible]

PT murine antibody NA-8, prevent binding of neutrophils to endothelial cells useful for treating inflammation

XX  
XX

[illegible]

CC chain and light chain variable domain genes of NA-8 were cloned

CC deduced AA sequences are shown in AAQ66845/R59509 and AAQ66846/R59510.

SQ Sequence 133 AA;

Query Match	82.28;	Score 559.5;	DB 15;	Length 133;
Best Local Similarity	80.58;	Pred. No. 2.8e-37;		
Matches 107; Conservative	15;	Mismatches 10;	Indels 1;	Gaps 1;

```
QY      1 MDSQAVLLELLMWSGTCGDIVLTQSPDLSAVSLGERATICKSSQSLNRPRENYLA 600
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
          1 mdsqavllmlllwsgtcgdvmsqspslavsvgekvmtscskssqsllysslqknyla 600
```

[illegible]

QY	121	-YTFGGTKEIK	132
		:       :	
Db	121	pftfgsgtkleik	133

RESULT 9  
 AAP80894  
 ID AAP80894 standard; protein; 133 AA.  
 AC AAP80894;  
 DT 03-DEC-1990 (first entry)  
 DE V region of L chain of anti-P.aeruginosa exotoxin Ab #1.  
 DE V region of L chain of anti-P.aeruginosa exotoxin Ab #1.  
 KM Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region;  
 KM ds.  
 OS Homo sapiens.  
 FH Key  
 FH Peptide 1..20  
 FT /label=signal peptide  
 FT Region 21..133  
 FT /label=V region of L chain  
 PN EP270077-A.  
 PD 08-JUN-1988.  
 PE 01-DEC-1987; 87EP-0117760.  
 PR 03-DEC-1986; 86JP-0288340.  
 PR 26-NOV-1987; 87JP-0298513.  
 PA (SDMO ) SUMITOMO CHEM IND KK.  
 PI Nakatani T, Nomura N, Horigome K, Noguchi H;  
 DR WPI: 1988-156310/23.  
 DR N-PSDB; AAN80499.  
 XX New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -  
 PT plus recombinant vectors and host cells, useful for treating  
 PT infections.  
 PS Claim 4; Page 25; 39pp; English.  
 CC Sequence is variable region of light chain of anti-exotoxin  
 CC antibody with signal sequence. AAN80498 encodes the same sequence  
 CC except that its signal peptide-encoding sequence contains an  
 CC intron.  
 CC See also AAN80495-N80496, AAN80498 and AAN80941-2.  
 CC  
 XX Sequence 133 AA;  
 SQ  
 Query Match 81.9%; Score 557.5; DB 9; Length 133;  
 Best Local Similarity 84.6%; Pred. No. 4.1e-37;  
 Matches 110; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

XX AAP06206;  
 AC 17-FEB-1997 (first entry)  
 DT Xenograft antibody HAR-1 kappa light chain variable region.  
 DE Xenograft rejection; xenotransplantation; organ transplant;  
 DE animal model; hamster; monoclonal antibody; HAR-1.  
 KM Rattus sp.  
 OS  
 FH Key  
 FH Region 1..20  
 FT /label= Leader  
 FT Region 21..43  
 FT /label= FR-1  
 FT /note= "framework region 1"  
 FT /label= CDR-1  
 FT /note= "complementarity determining region 1"  
 FT 61..75  
 FT /label= FR-2  
 FT /note= "framework region 2"  
 FT 76..82  
 FT /label= CDR-2  
 FT /note= "complementarity determining region 2"  
 FT 83..114  
 FT /label= FR-3  
 FT /note= "framework region 3"  
 FT 115..122  
 FT /label= CDR-3  
 FT /note= "complementarity determining region 3"  
 FT 123..134  
 FT /label= FR-4  
 FT /note= "framework region 4"  
 PN WO9636358-A1.  
 PD 21-NOV-1996.  
 PR 14-MAY-1996; 96WO-US06804.  
 PR 15-MAY-1995; 95US-0440621.  
 PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
 PI Cramer DV, Makowka L, Wu G;  
 DR WPI: 1997-011852/01.  
 DR N-PSDB; AAT43415.  
 XX Inhibiting xenograft rejection by modifying antigen expression of  
 PT the graft - prevents binding of anti-donor antibody and prolongs  
 PT graft survival  
 PS Claim 11; Page 99; 135pp; English.  
 CC A polypeptide (AAP06206) comprises the kappa light chain variable  
 CC region of the LEW rat anti-hamster xenograft monoclonal antibody  
 CC HAR-1. It is encoded by a cDNA clone (AAT43415) obtd. from a HAR-1  
 CC hybridoma light chain cDNA library; the hybridoma was produced by  
 CC fusing spleen cells of a LEW rat that had received a hamster heart  
 CC transplant, with rat myeloma cells. Recombinant fragments, e.g.  
 CC (Fab')2 and Fab', of the antibody block binding of preformed  
 CC anti-donor xenograft antibodies in a recipient animal serum to  
 CC antigen expressed by endothelial cells of the xenograft, i.e. they  
 CC inhibit antibody-mediated rejection, thereby prolonging the  
 CC survival of the hamster xenograft in the recipient.  
 CC  
 XX Sequence 134 AA;  
 SQ







```

XX      WO9209305-A.
PN
XX      11-JUN-1992.
PD
XX      27-NOV-1991; 91WO-US08843.
PF
XX      27-NOV-1990; 90US-0618542.
PR
XX      (BIOJ ) BIOGEN INC.
PA
XX      Burkle LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
PI      MPI: 1992-39839/48.
DR      N-PSDB; AAQ30920.
XX
XX      New anti-CD4 antibody homologues - which bind CD4, do not block
PT      binding of HIV gp120 to CD4 but block HIV-induced syncytia
PR      formation between CD4+ cells
XX
XX      Disclosure: Page 166-7; 205pp; English.
PS
XX
XX      The sequence given is encoded by the insert of the vector pMDR1007.
CC      pMDR1006 (see AAQ30919) and pSAB132 (see AAQ30906) were used in the
CC      construction of this vector. Three fragments were ligated together
CC      to generate pMDR1006; a 572 bp fragment of pMDR85 (see AAQ30913), a
CC      3442bp ActI/EcoRV fragment of pMDR986 (see AAQ30918) and a 326 bp
CC      EcoRV/BglII fragment of pMDR1003 (see AAQ30900). The ligation mixture
CC      was used to transform E. coli JA221(Iq) to ampicillin resistance.
CC      pMDR1006 was cleaved with NotI and the 1693 bp fragment isolated
CC      was ligated into NotI linearised pSAB132 which had been dephosphorylated
CC      by calf alkaline phosphatase. This generates the plasmid pMDR1007.
CC      The dephosphorylated mixture was fractionated through low temperature
CC      melting agarose and used to transform E. coli JA221(Iq) to ampicillin
CC      resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'
CC      order, the immunoglobulin kappa chain signal peptide, amino acid (AA)
CC      1-AA112 of the humanised 5A8 light chain variable region (LV) followed
CC      by genomic DNA encoding AA108-AA214 of the human kappa light chain,
CC      ie. the light chain constant region (LC). This polypeptide is an
CC      antibody homolog which was shown to bind to CD4 but did not block the
CC      binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+
CC      lymphocytes (helper/inducer cells). The homolog blocked HIV-induced
CC      syncytia formation. This homolog can be used in the detection,
CC      prophylaxis and treatment of diseases caused by infective agents whose
CC      primary targets are CD4+ cells.
CC
XX      Sequence 241 AA:
SQ

```

```

Query Match      80.5%; Score 548; DB 13; Length 241;
Best Local Similarity 83.6%; Pred. No. 4.1e-36;
Matches 107; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

```

```

OY      5 AOVLLILLWAGTGGDYLITLSPDSLAVSLGPRATISCKSSQSLNRTRENYLAWYQ 64
      ||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      7 aqlllqlllllwpragaydlwmcgsdplawslgeratincssqsllystnqkylawyq 66
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      65 KRQGPKKLLIYASTRESGVPDRFSGSGSGTFTLTISSLQAEDVAIVYVYCTQSYNLTFFG 124
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      67 kpgqpklllywastresgvpdrfsgsgsgtftltlsslqaedvayvyqgyysrtffg 126
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY      125 QGTKEIK 132
      :|||:|
DB      127 rgtkleik 134

```

```

RESULT 15
AAV50161
ID      AAV50161 standard; Protein: 240 AA.
XX
AC      AAV50161;
XX
DT      31-JAN-2000 (first entry)

```

```

XX      Human reshaped F19 antibody light chain (version a).
DE
XX
XX      Antibody; monoclonal; F19; fibrinogen activation protein alpha; PAP;
KW      humanisation; complementarity determining region; CDR; CDR grafting;
KW      reshaped; reactive stroma; fibroblast; epithelial cancer;
KW      diagnosis; immune response; framework sequence; constant region;
KW      variable region; productibility; treatment; cancer; colorectal; lung;
KW      breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis;
KW      detection; wound healing; skin inflammation; tumour; immunogenicity;
XX      chimeric; light chain.
XX
XX      Chimeric - Mus sp.
OS
XX      Chimeric - Homo sapiens.
XX
XX      Key
FH      Location/Qualifiers
FT      Peptide
FT      1..20
FT      /note= "Leader peptide"
FT      Protein
FT      21..240
FT      /note= "Mature human reshaped F19 light chain"
FT      Region
FT      21..140
FT      /note= "Mature reshaped human F19 light chain variable
FT      region"
FT      Region
FT      44..60
FT      /note= "Complementarity determining region (CDR) 1"
FT      Region
FT      76..82
FT      /note= "CDR 2"
FT      Region
FT      115..123
FT      /note= "CDR 3"
FT      Region
FT      141..240
FT      /note= "human kappa light chain constant region"
XX
XX      EP953639-A1.
XX      03-NOV-1999.
XX      30-APR-1998; 98EP-0107925.
XX      30-APR-1998; 98BP-0107925.
XX      (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX      Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
PI      Rettig WJ;
XX
XX      MPI: 1999-621833/54.
DR      N-PSDB; AA232784.
XX
XX      New antibody protein, useful for treating cancer and for imaging
PT      presence of activated stromal fibroblasts in healing wound or inflamed
PT      skin -
XX
XX      Example 3; Fig 30; 143pp; English.
PS
XX
XX      This sequence represents the light chain (version a) of a reshaped human
CC      F19 antibody. F19 (ATCC Accession number HB 8265) is a murine monoclonal
CC      antibody against fibroblast activation protein alpha (FAP). FAP is a cell
CC      surface molecule of reactive stromal fibroblasts, and its induction
CC      is a highly consistent molecular trait of the reactive stroma of many
CC      types of epithelial cancer. Although F19 may be useful in vitro, e.g.,
CC      for diagnosis, its applications for in vivo use in humans are problematic
CC      as it elicits a human anti-mouse response which reduces the efficacy of
CC      the antibody in patients and impairs continued administration. The
CC      novel human reshaped F19 was humanised by grafting the murine
CC      complementarity determining regions (CDRs) of F19 onto human variable
CC      region framework sequences, and then joining these "reshaped human"
CC      variable regions to human constant regions. These modifications
CC      also result in the improved producibility in eukaryotic cell culture
CC      systems as compared to a chimeric antibody having the entire variable
CC      regions of F19 joined to human constant regions. The human reshaped F19
CC      antibody has low immunogenicity for humans and is useful for treating
CC      cancers e.g., colorectal cancers, non-small cell lung cancers, breast
CC      cancers, head and neck cancers, ovarian cancers, lung cancers, bladder
CC

```



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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:00:19 ; Search time 20.74 Seconds

(without alignments)  
155,457 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681

Sequence: 1 MDSQAQVILILLMWSTGTCG.....YCTOSYLNLYTGGTKVEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
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4: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfileseq.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	592	86.9	239	1	US-08-353-400-37
2	553.5	81.3	135	3	US-08-812-586-46
3	548.5	80.5	133	3	US-08-463-903-4
4	548.5	80.5	133	4	US-07-935-695-4
5	548	80.5	241	2	US-07-916-098A-56
6	528.5	77.6	133	2	US-08-822-028-12
7	528.5	77.6	133	2	US-08-479-285-12
8	526.5	77.3	133	5	PCT-US93-11611-2
9	522.5	76.7	154	3	US-08-513-968-36
10	513.5	75.4	495	3	US-08-828-741B-4
11	513.5	75.4	495	4	US-09-160-567-4
12	512.5	75.3	133	4	US-08-579-378A-2
13	512.5	75.3	133	5	PCT-US93-11612-2
14	512.5	73.8	113	4	US-08-525-539A-80
15	502.5	73.8	155	3	US-08-828-741B-11
16	502.5	73.8	155	4	US-09-160-567-11
17	502.5	73.8	342	3	US-08-828-741B-6
18	502.5	73.8	342	4	US-09-160-567-6
19	500.5	73.5	114	4	US-09-025-769B-17
20	498.5	73.2	113	5	PCT-US93-08435-8
21	498.5	73.2	275	4	US-08-463-903-6
22	498.5	73.2	275	4	US-09-935-695-6
23	497.5	73.1	115	4	US-09-025-769B-31
24	497.5	73.1	115	4	US-09-025-769B-31
25	496.5	72.9	114	1	US-08-360-125-6
26	496.5	72.9	114	2	US-08-450-578-6
27	496.5	72.9	114	2	US-09-017-628-6

28	496.5	72.9	114	2	US-09-014-880-6	Sequence 6, App1
29	496	72.8	112	1	US-07-942-245-30	Sequence 30, App1
30	494.5	72.6	171	3	US-08-463-903-20	Sequence 20, App1
31	494.5	72.6	171	4	US-07-935-695-20	Sequence 20, App1
32	494	72.5	114	4	US-08-929-856-66	Sequence 66, App1
33	491.5	72.2	134	5	PCT-US93-11611-9	Sequence 9, App1
34	490.5	72.0	113	5	PCT-US93-08435-6	Sequence 6, App1
35	490	72.0	219	1	US-08-353-400-34	Sequence 34, App1
36	489.5	71.9	285	3	US-08-463-903-22	Sequence 22, App1
37	489.5	71.9	285	4	US-07-935-695-22	Sequence 22, App1
38	488.5	71.7	134	4	US-08-718-323A-4	Sequence 4, App1
39	487.5	71.6	260	3	US-08-463-903-2	Sequence 2, App1
40	487.5	71.6	260	4	US-07-935-695-2	Sequence 2, App1
41	487	71.5	288	4	US-09-423-439-38	Sequence 38, App1
42	487	71.5	673	4	US-09-423-439-32	Sequence 32, App1
43	485.5	71.3	113	1	US-08-467-420A-21	Sequence 21, App1
44	485.5	71.3	113	1	US-08-470-110A-21	Sequence 21, App1
45	485.5	71.3	113	1	US-08-667-769A-21	Sequence 21, App1

## ALIGNMENTS

RESULT 1  
US-08-353-400-37  
Sequence 37, Application US/08353400  
Patent No. 5665357  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-37

Query Match 86.9%, Score 592, DB 1, Length 239;  
Best local Similarity 84.8%; Pred. No. 4.5e-48;  
Matches 112; Conservative 11; Mismatches 9; Indels 0; Caps 0;

QY 1 MDSQAQVILILLMWSTGCGIVYLTQSPDSLAVSLGERATISCKSSQSLNSRRRENTLA 60  
|||||  
DB 1 MDSQAQVILILLMWSTGCGIVMSQSPSSLAAGKVTYMSCKSSQSLNSRRRKNLA 60  
QY 61 WYQOKPOPEKLLIYMASTRESGVDPDRFGSGSGSTDFLTFTSSLOAEDVAVYCTQSYNL 120  
|||||  
DB 61 WYQORPOSPKRLIYMASTRTSGVDPDRFTGSGSGTDFLTFTSSVOAEDLAITYCKOSTYL 120  
QY 121 YTFGGTKVEIK 132  
|||||  
DB 121 YTFGGTKVEIK 132

```

RESULT      2
US-08-812-586-46
: Sequence 46, Application US/08812586
: Patent No. 6048704
: GENERAL INFORMATION:
: APPLICANT: Martin David Nilson
: TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
: TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
: TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
: NUMBER OF SEQUENCES: 61
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/812,586
: FILING DATE: 07-MAR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28, 678
: REFERENCE/DOCKET NUMBER: 0575/53862-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: INFORMATION FOR SEQ ID NO: 46:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 135 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-812-586-46

Query Match      81.3%; Score 553.5; DB 3; Length 135;
Best Local Similarity 84.6%; Pred. No. 9,3e-45;
Matches 110; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY      4 QAAVILLLLLSGTCGDIYLTQSPDSLAVSLGERATITSCSSQSLLNSTRENYLAWYQ 63
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4 QTVQVLSILMTLSGAAGDLYMTQSPDSLAVSLGERATITNKSSQSLLYSSNNKRYLAWYQ 63
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      64 QKGGPPKLLIYWASTRRESGVDPDRFSGSGSGTDFTLTISLSLAEDVAVYVYCTQSYNLT 122
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      64 QKGGPPKLLIYWASTRRESGVDPDRFSGSGSGTDFTLTISLSLAEDVAVYVYCTQSYNLT 123
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      123 FGQGTKEIK 132
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      124 FGQGTKEIK 133
      1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      3
US-08-463-903-4
: Sequence 4, Application US/08463903
: Patent No. 6071515
: GENERAL INFORMATION:
: APPLICANT: Mezes, Peter S.
: APPLICANT: Richiard, Ruth A.
: APPLICANT: Affholter, Joseph A.
: APPLICANT: Koltze, Nicolas J.
: TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
: FILE REFERENCE: 40224A US
: CURRENT APPLICATION NUMBER: US/08/463,903
: CURRENT FILING DATE: 1995-06-05

```

```

EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 4
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from prl1001
LOCATION: 1..133
US-08-463-903-4

Query Match      80.5%   Score 548.5; DB 3; Length 133;
Best Local Similarity 83.8%; Pred. No. 2.7e+44;
Matches 109; Conservative 6; Mismatches 14; Indels 1; Gaps 1.

QY    4 OAOVILLILMWSTGCGIVLTSPDLSLAVSLGERATISCKSSOSILNSRPRENYLAWQ 63
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db    4 QTOVLISLLMTISAGVDIWMQTGSDLSLVSGERATINCKSSQSVLSNNKNYLAWQ 63

OY    64 OKPGOPKULLIYWASTRESGVDRPDRSGSGGTDFLLTSSLOAEVAYVYCQTQSYNL-YT 122
      | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db    64 OKPGOPKULLIYWASTRESGVDRPDRSGSGGTDFLLTSSLOAEVAYVYCOOYYSTPLT 123

OY    123 FGOGTKVEIK 132
      ||| |||| |
Db    124 FGGGTKVAIK 133

```

Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length
80.5%	83.8%	6	14	Indels	1	Gaps
109						
US-07-935-695-4						
Sequence 4, Application US/07935695						
Patent No. 6329507						
GENERAL INFORMATION:						
APPLICANT: Mezes, Peter S.						
APPLICANT: Richard, Ruth A.						
APPLICANT: Affholter, Joseph A.						
APPLICANT: Kotite, Nicolas J.						
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides						
FILE REFERENCE: 40224 US						
CURRENT APPLICATION NUMBER: US/07/935,695						
CURRENT FILING DATE: 1992-08-21						
PRIOR APPLICATION NUMBER: US 08/463,903						
PRIOR FILING DATE: 1995-06-05						
NUMBER OF SEQ ID NOS: 102						
SOFTWARE: MS-Word for Windows, Ver. 7.0						
SEQ ID NO 4						
LENGTH: 133						
TYPE: PRT						
ORGANISM: Homo sapiens						
FEATURE:						
NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001						
LOCATION: 1..133						
US-07-935-695-4						
Query Match	80.5%	Score 548.5	DB 4	Length 133		
Best Local Similarity	83.8%	Pred. No. 2.7e-44				
Matches 109	Conservative	6	Mismatches 14	Indels	1	Gaps
1						
US-07-935-695-4						
Sequence 4, Application US/07935695						
Patent No. 6329507						
GENERAL INFORMATION:						
APPLICANT: Mezes, Peter S.						
APPLICANT: Richard, Ruth A.						
APPLICANT: Affholter, Joseph A.						
APPLICANT: Kotite, Nicolas J.						
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides						
FILE REFERENCE: 40224 US						
CURRENT APPLICATION NUMBER: US/07/935,695						
CURRENT FILING DATE: 1992-08-21						
PRIOR APPLICATION NUMBER: US 08/463,903						
PRIOR FILING DATE: 1995-06-05						
NUMBER OF SEQ ID NOS: 102						
SOFTWARE: MS-Word for Windows, Ver. 7.0						
SEQ ID NO 4						
LENGTH: 133						
TYPE: PRT						
ORGANISM: Homo sapiens						
FEATURE:						
NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001						
LOCATION: 1..133						
US-07-935-695-4						
Query Match	80.5%	Score 548.5	DB 4	Length 133		
Best Local Similarity	83.8%	Pred. No. 2.7e-44				
Matches 109	Conservative	6	Mismatches 14	Indels	1	Gaps
1						
US-07-935-695-4						
Sequence 4, Application US/07935695						
Patent No. 6329507						
GENERAL INFORMATION:						
APPLICANT: Mezes, Peter S.						
APPLICANT: Richard, Ruth A.						
APPLICANT: Affholter, Joseph A.						
APPLICANT: Kotite, Nicolas J.						
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides						
FILE REFERENCE: 40224 US						
CURRENT APPLICATION NUMBER: US/07/935,695						
CURRENT FILING DATE: 1992-08-21						
PRIOR APPLICATION NUMBER: US 08/463,903						
PRIOR FILING DATE: 1995-06-05						
NUMBER OF SEQ ID NOS: 102						

```

RESULT      5
US-07-916-098A-56
Sequence 56, Application US/07916098A
Patent No. 5871732
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: JULY 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: NO. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-916-098A-56

Query Match          80.5%; Score 548; DB 2; Length 241;
Best Local Similarity 83.6%; Pred. No. 5.8e-44;
Matches 107; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY    5 AQLVILLILWVSGTCGDIVLTQSPDSLAVSLGERATTSCKSSQSLNSRTRENYLAWYQQ 64
      |||:|||||: | ||||:|||||:|||||:|||||: ||| | :|||:|||||
Db    7 AQLGLGILLMLPAGRGDIVMTQSPDSLAVSLGERATINCKSSGISLVSTNQKNYLAWYQQ 66
      KPGGPRLIIYWASTRESGVDPFRSGSGSGNDPFTLTSSLAQPAVAYVYYCCQSYNLRYFG 124
      67 KPGGPRLIIYWASTRESGVDPFRSGSGSGNDPFTLTSSLAQPAVAYVYYCCQSYNYRTEG 126
QY    125 QGTVEIK 132
      :|||:|||
Db    127 RGTKLEIK 134

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US-08-822-028-12
: Sequence 12, Application US/08822028
: Patent No. 5993813
: GENERAL INFORMATION:
: APPLICANT: MEZES, PETER S
: APPLICANT: GOURLIE, BRIAN B
: APPLICANT: RIXON, MARK W
: APPLICANT: ANDERSON, WH KERR
: APPLICANT: KAPLAN, DONALD A
: APPLICANT: SCHOLON, JEFFREY
: TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
: TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
: NUMBER OF SEQUENCES: 74
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DUANE C ULMER
: STREET: P. O. BOX 1967
: CITY: MIDLAND
: STATE: MICHIGAN
: COUNTRY: USA
: ZIP: 48641-1967
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/822.028
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/040,687
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: ULMER, DUANE C
: REGISTRATION NUMBER: 34,941
: REFERENCE/DOCKET NUMBER: C-37, 075C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (517) 636-8104
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 133 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-822-028-12

Query Match 77.6%; Score 528.5; DB 2; Length 133;
Best Local Similarity 75.9%; Pred. No. 2e-42;
Matches 101; Conservative 16; Mismatches 15; Indels 1; Gaps 1;

QY 1 MDSQAQVILLILLWVSGTCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENTYA 60
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDSQAQVILLILLWVSGTCGDIVMSQSPSSLPVSVEKVTLSCKSSQSLNSTRRENTYA 60
QY 61 WYQOKPGGPKRLIYWASTRSGVDFRFGSGSGGTDFLTLLISSLAEDPAVAVYCTQSYNL 120
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 WYQOKPGGSPKRLIYWASARSGVDFRFTGSGGTDFLTLLISSVKTEDLAVYCCQYISY 120
QY 121 -YTFGGTGKVEIK 132
: |||||:|
Db 121 PLTFGAGTKVLVK 133

RESULT 7
US-08-479-285-12
: Sequence 12, Application US/08479285
: Patent No. 6207815
: GENERAL INFORMATION:
: APPLICANT: MEZES, PETER S
: APPLICANT: GOURLIE, BRIAN B
: APPLICANT: RIXON, MARK W
: APPLICANT: ANDERSON, WH KERR

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```

1  APPLICANT: DO COUTO, FERNANDO J. R.
2  APPLICANT: CERIANI, ROBERTO L.
3  APPLICANT: PETERSON, JERRY A.
4  TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
5  TITLE OF INVENTION: M3 ANTI-B46 ANTIBODY, METHODS OF USE THEREOF, AND
6  TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
7  NUMBER OF SEQUENCES: 81
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE: MORRISON & FOERSTER
10 STREET: 755 Page Mill Road
11 City: Palo Alto
12 STATE: CA
13 COUNTRY: USA
14 ZIP: 94304-1018
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/525,539A
23 FILING DATE: 14-SEP-1995
24 CLASSIFICATION: 424
25 ATTORNEY/AGENT INFORMATION:
26 NAME: DYLAN, TYLER
27 REGISTRATION NUMBER: 37,612
28 REFERENCE/DOCKET NUMBER: 27633-20001.21
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (415) 813-5600
31 TELEFAX: (415) 494-0792
32 TELEX: 706141
33 INFORMATION FOR SEQ ID NO: 80:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 113 amino acids
36 TYPE: amino acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39
40 US-08-525-539A-80
41
42 Query Match 73.8%; Score 502.5; DB 4; Length 113;
43 Best Local Similarity 87.6%; Pred. NO. 4.3e-40;
44 Matches 99; Conservative 5; Mismatches 8; Indels 1; Gaps 1;
45
46 QY 21 DIVLQSPDSLAVSGERATISCKSSQSILNSRTRENTLAWYQKPGPKLLIYMASTR 80
47 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
48 Db 1 DIVMGPDSLAVSLGERRATINCKSSQSVIVSSNNKNITLAWYQKPGPKLLIYMASTR 60
49
50 QY 81 ESGVDPRSGSGSGTDFLTLLTSSLDQEDVAVYYCTQSTNL-VTFSGGTVEIK 132
51 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
52 Db 61 ESGVDPRSGSGSGTDFLTLLTSSLDQEDVAVYYCOQYSTPTFGQGTVEIK 113
53
54 RESULT 15
55 US-08-828-741B-11
56 Sequence 11, Application US/08828741B
57 Patent No. 6043069
58 GENERAL INFORMATION:
59 APPLICANT: Koentgen, Frank
60 APPLICANT: Suess, Gabriele M.
61 APPLICANT: Tarlinton, David M.
62 APPLICANT: Treutlein, Herbert R.
63 TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
64 TITLE OF INVENTION: PRODUCING SAME
65 NUMBER OF SEQUENCES: 14
66 CORRESPONDENCE ADDRESS:
67 ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
68 STREET: 400 Garden City Plaza
69 City: Garden City
70 STATE: New York
71 COUNTRY: United States of America
72 ZIP: 11530
73 COMPUTER READABLE FORM:

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1  MEDIUM TYPE: Floppy disk
2  COMPUTER : IBM PC compatible
3  OPERATING SYSTEM: PC-DOS/MS-DOS
4  SOFTWARE: PatentIn Release #1.0, Version #1.30
5  CURRENT APPLICATION DATA:
6  APPLICATION NUMBER: US/08/828,741B
7  FILING DATE: 26-MAR-1997
8  CLASSIFICATION: 435
9  ATTORNEY/AGENT INFORMATION:
10 NAME: Digiglio, Frank S.
11 REGISTRATION NUMBER: 31,346
12 REFERENCE/DOCKET NUMBER: 10591
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (516) 742-4343
15 TELEFAX: (516) 742-4366
16 TELEX: 230 901 SANS UR
17 INFORMATION FOR SEQ ID NO: 11:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 155 amino acids
20 TYPE: amino acid
21 TOPOLOGY: linear
22 MOLECULE TYPE: protein
23
24 US-08-828-741B-11

```

Query Match	73.8%	Score 502.5	DB 3	Length 155
Best Local Similarity	86.7%	Pred. No. 6.1e-40		
Matches	98	Conservative	7	Mismatches 7; Indels 1; Gaps 1
QY	21	DIVLRQSPDSLAVSLGGERATISCKSSQSLNTRTENTYLAWYQKPGPKLLIYASTR	80	
		:     :     :     : :     :     :     :     :     :     :		
Db	30	DIVMFOSPDSLAVSLGGERATINCKSSQSLVYSSNSKNITLAWYQKPGPKLLIYASTR	89	
QY	81	ESGVDFRFGSGSGGTFLLTILISLQAEADVAVYVCTQSYNL-ITFGGCTVETIK	132	
		:     :     :     :     :     :     :     :     :     :		
Db	90	ESGVDFRFGSGSGGTFLLTILISLQAEADVAVYVCTQSYNTPYSGGCTVETIK	142	

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Search completed: August 26, 2002, 15:00:20
Job time: 154 sec
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